Serial No.: 08/866,354

Page 11, line 31, after "(rat GRR3)" insert --(SEQ ID NO: 42)--.

Page 12, line 1, after "sequence" insert -(SEQ ID NO: 43)--.

Page 12, line 25, after "consensus sequence" insert -- (SEQ ID NO: 44)--.

Page 98, line 18, after "Figure 26" insert -- (SEQ ID NO: 44)--.

Page 98, line 30, after "Figure 26" insert -- (SEQ ID NO: 44)--.

REMARKS

As described above, the specification has been amended so that the figures are more clearly referenced by the appropriate sequence identification numbers. The amendments are fully supported by the specification, and no new matter has been added.

Respectfully submitted,

David R. Com

Daniel R. Curry

Attorney for Applicants Registration No.: 32,727 Phone: (805) 447-8102

Date: April 6, 1998

Please send all future correspondence to:

U.S. Patent Operations/DRC Dept. 430, M/S 27-4-A AMGEN INC. One Amgen Center Drive Thousand Oaks, California 91320-1789

45

SEOUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: Fox, Gary M Jing, Shuqian Wen, Duanzhi
 - (ii) TITLE OF INVENTION: NEUROTROPHIC FACTOR RECEPTORS
 - (iii) NUMBER OF SEQUENCES: 44
 - (iv) CORRESPONDENCE ADDRESS:

 - (A) ADDRESSEE: AMGEN INC(B) STREET: One Amgen Center Drive
 - (C) CITY: Thousand Oaks
 - (D) STATE: CA

 - (E) COUNTRY: US (F) ZIP: 91320-1789
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk

 - (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/866,354
 - (B) FILING DATE: 30-MAY-1997
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/837,199
 - (B) FILING DATE: 14-APR-1997
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/015,907
 - (B) FILING DATE: 22-APR-1996
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/017,221
 - (B) FILING DATE: 09-MAY-1996
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Curry, Daniel R.
 - (B) REGISTRATION NUMBER: 32,727
 - (C) REFERENCE/DOCKET NUMBER: A-401B
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2568 base pairs(B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:

 - (A) NAME/KEY: CDS
 (B) LOCATION: 540..1934

a

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

			•									J	20011	יייי	(11.11)	
60	CCTAA	CATO	CTA A	ACCAC	ATA	rcca	CGCTT	GC(rccgo	ATTC	GC C	ACAC	CGGA	CCT (CTGG	AATO
120	TTCGAG	CCCI	rcg (CAACI	GCC	CCTG	rcgto	A AA	rcggz	CTGC	GC T	GAGG	AGCC	CCG 2	CATO	CGA
180	AGATAA	CGC	CTA (TTTC	TCTT	TTTT	CTTT	TTC	PTTT	ATTT:	TC T	CGCA'	TAC	AGA 1	rcga/	CTC
240	AATAAG	ATA	AAG A	CTGA	GCC	CATT	ACAC	G GGZ	GCG	AGGG	AG G	GGGA	GAAA	CCG (SAGC	AGT
300	TTGGGT	CAGGT	GTC (rtgac	CGG	CGGT	GACG	TG	GCAG	CGCC	CC T	GGCT	AACTO	ACA A	AATA	TAA
360	GAGTCG	AGCTO	CGG 2	ATCC	GCC	CCTC	CCGC	C TC	CCGC	GGAA	AG C	raaa.	cccr	GAA (ACCTO	CGGZ
420	rgaact	SAGCT	ATG (CTGGA	TCAC	TCTT	rtcc:	A GT	CCGG	AGAC	GC C	rgcT(rggc'	CGG !	GCGG	CCG
480	CGGCAA	CCTC	GCT (CTGAC	ACG	CTGC	ATCG	G GG	rccgo	GCTG:	AC A	CAGC	AGAG	GCC 2	GCG	TTG
539	GCACC	CCG	CGC (GCCC	CCAC	GGGA	GCG	G GG	rtgg(TTTT?	GA T	rcgg(CGGC	CGG (CCAG	GAC
587	CTC Leu	TTG Leu 15	GAC Asp	TTG Leu	CTC Leu	CCG Pro	CTG Leu 10	GCG Ala	TTC Phe	TAC Tyr	CTG Leu	ACC Thr 5	GCG Ala	CTG Leu	TTC Phe	ATG Met 1
635	GCC Ala	AAA Lys	GTG Val 30	TGC Cys	GAT Asp	CTG Leu	CGC Arg	GAC Asp 25	GGA Gly	GGC Gly	AGC Ser	GTG Val	GAA Glu 20	GCC Ala	TCG Ser	CTG Leu
683	ACG Thr	CGC Arg	TAC Tyr	AAG Lys 45	ACC Thr	AGC Ser	TGC Cys	AGC Ser	CAG Gln 40	GAG Glu	AAG Lys	CTG Leu	TGC Cys	CAG Gln 35	GAT Asp	AGT Ser
731	TCC Ser	GCA Ala	CTG Leu	AGC Ser	TTC Phe 60	AAC Asn	ACC Thr	GAG Glu	AAG Lys	GGC Gly 55	GCG Ala	GTG Val	TGC Cys	CAG Gln	AGG Arg 50	CTA Leu
779	AAG Lys 80	CTG Leu	GCC Ala	GAG Glu	ATG Met	GCC Ala 75	AGC Ser	CGC Arg	TGC Cys	GAG Glu	GAT Asp 70	AAG Lys	GCC Ala	GAG Glu	CTG Leu	GGC Gly 65
827	GAG Glu	AAG Lys 95	AAG Lys	ATG Met	GGT Gly	CGG Arg	AAG Lys 90	TGC Cys	CGC Arg	TGC Cys	AAC Asn	TAC Tyr 85	CTC Leu	TCG Ser	AAG Lys	CAG Gln
875	GGA Gly	CAG Gln	CTG Leu 110	AGC Ser	CAG Gln	TAC Tyr	ATG Met	AGC Ser 105	TGG Trp	TAC Tyr	ATT Ile	CGC Arg	CTG Leu 100	TGC Cys	AAC Asn	AAG Lys
923	TTG Leu	AGA Arg	AGC Ser	AAC Asn 125	GTT Val	CCA Pro	GAA Glu	TAT Tyr	CCA Pro 120	TCC Ser	GAT Asp	GAG Glu	CTG Leu	CTG Leu 115	GAT Asp	AAT Asn
971	CAA Gln	CAG Gln	TTT Phe	GTT Val	GAT Asp 140	TCA Ser	ATA Ile	TTC Phe	CCA Pro	GTC Val 135	GTG Val	CGG Arg	TTC Phe	ATA Ile	GAT Asp 130	TCA Ser
1019	GCC Ala 160	AAG Lys	GCG Ala	GCA Ala	GAT Asp	CTG Leu 155	TGC Cys	AAC Asn	AAC Asn	GGG Gly	AAA Lys 150	CCC Pro	ATT Ile	CAC His	GAG Glu	GTG Val 145
1067	ACC Thr	ATC Ile	TAC Tyr	GCG Ala	TCG Ser	AGG Arg	TAC Tyr	AAG Lys	AAG Lys	TGC Cys	ATT Ile	GAC Asp	GAC Asp	CTC Leu	AAC Asn	TGC Cys

				165					170					175		
CCG Pro	TGC Cys	ACC Thr	ACC Thr 180	AGC Ser	GTG Val	TCC Ser	AAC Asn	GAT Asp 185	GTC Val	TGC Cys	AAC Asn	CGC Arg	CGC Arg 190	AAG Lys	TGC Cys	1115
CAC His	AAG Lys	GCC Ala 195	CTC Leu	CGG Arg	CAG Gln	TTC Phe	TTT Phe 200	GAC Asp	AAG Lys	GTC Val	CCG Pro	GCC Ala 205	AAG Lys	CAC His	AGC Ser	1163
TAC Tyr	GGA Gly 210	ATG Met	CTC Leu	TTC Phe	TGC Cys	TCC Ser 215	TGC Cys	CGG Arg	GAC Asp	ATC Ile	GCC Ala 220	TGC Cys	ACA Thr	GAG Glu	CGG Arg	1211
AGG Arg 225	CGA Arg	CAG Gln	ACC Thr	ATC Ile	GTG Val 230	CCT Pro	GTG Val	TGC Cys	TCC Ser	TAT Tyr 235	GAA Glu	GAG Glu	AGG Arg	GAG Glu	AAG Lys 240	1259
CCC Pro	AAC Asn	TGT Cys	TTG Leu	AAT Asn 245	TTG Leu	CAG Gln	GAC Asp	TCC Ser	TGC Cys 250	AAG Lys	ACG Thr	AAT Asn	TAC Tyr	ATC 11e 255	TGC Cys	1307
AGA Arg	TCT Ser	CGC Arg	CTT Leu 260	GCG Ala	GAT Asp	TTT Phe	TTT Phe	ACC Thr 265	AAC Asn	TGC Cys	CAG Gln	CCA Pro	GAG Glu 270	TCA Ser	AGG Arg	1355
TCT Ser	GTC Val	AGC Ser 275	AGC Ser	TGT Cys	CTA Leu	AAG Lys	GAA Glu 280	AAC Asn	TAC Tyr	GCT Ala	GAC Asp	TGC Cys 285	CTC Leu	CTC Leu	GCC Ala	1403
TAC Tyr	TCG Ser 290	GGG Gly	CTT Leu	ATT Ile	GGC Gly	ACA Thr 295	GTC Val	ATG Met	ACC Thr	CCC Pro	AAC Asn 300	TAC Tyr	ATA Ile	GAC Asp	TCC Ser	1451
AGT Ser 305	AGC Ser	CTC Leu	AGT Ser	GTG Val	GCC Ala 310	CCA Pro	TGG Trp	TGT Cys	GAC Asp	TGC Cys 315	AGC Ser	AAC Asn	AGT Ser	GGG Gly	AAC Asn 320	1499
GAC Asp	CTA Leu	GAA Glu	GAG Glu	TGC Cys 325	TTG Leu	AAA Lys	TTT Phe	TTG Leu	AAT Asn 330	TTC Phe	TTC Phe	AAG Lys	GAC Asp	AAT Asn 335	ACA Thr	1547
TGT Cys	CTT Leu	AAA Lys	AAT Asn 340	GCA Ala	ATT Ile	CAA Gln	GCC Ala	TTT Phe 345	GGC Gly	AAT Asn	GGC Gly	TCC Ser	GAT Asp 350	GTG Val	ACC Thr	1595
GTG Val	TGG Trp	CAG Gln 355	CCA Pro	GCC Ala	TTC Phe	CCA Pro	GTA Val 360	CAG Gln	ACC Thr	ACC Thr	ACT Thr	GCC Ala 365	ACT Thr	ACC Thr	ACC Thr	1643
ACT Thr	GCC Ala 370	CTC Leu	CGG Arg	GTT Val	AAG Lys	AAC Asn 375	AAG Lys	CCC Pro	CTG Leu	GGG Gly	CCA Pro 380	GCA Ala	GGG Gly	TCT Ser	GAG Glu	1691
AAT Asn 385	GAA Glu	ATT Ile	CCC Pro	ACT Thr	CAT His 390	GTT Val	TTG Leu	CCA Pro	CCG Pro	TGT Cys 395	GCA Ala	AAT Asn	TTA Leu	CAG Gln	GCA Ala 400	1739
CAG Gln	AAG Lys	CTG Leu	AAA Lys	TCC Ser 405	AAT Asn	GTG Val	TCG Ser	GGC Gly	AAT Asn 410	ACA Thr	CAC His	CTC Leu	TGT Cys	ATT Ile 415	TCC Ser	1787
AAT Asn	GGT Gly	AAT Asn	TAT Tyr	GAA Glu	AAA Lys	GAA Glu	GGT Gly	CTC Leu	GGT Gly	GCT Ala	TCC Ser	AGC Ser	CAC His	ATA Ile	ACC Thr	1835

	420	425	430	
ACA AAA TCA Thr Lys Ser 435	ATG GCT GCT CCT Met Ala Ala Pro	CCA AGC TGT GGT Pro Ser Cys Gly 440	CTG AGC CCA CTG CTG Leu Ser Pro Leu Leu 445	1883
GTC CTG GTG Val Leu Val 450	GTA ACC GCT CTG Val Thr Ala Leu 455	Ser Thr Leu Leu	TCT TTA ACA GAA ACA Ser Leu Thr Glu Thr 460	1931
TCA TAGCTGC Ser 465	АТТ ААААААТАС А	ATATGGACA TGTAAAA	AGA CAAAAACCAA	1984
GTTATCTGTT	TCCTGTTCTC TTGTA	TAGCT GAAATTCCAG	TTTAGGAGCT CAGTTGAGA	AA 2044
ACAGTTCCAT	TCAACTGGAA CATTT	TTTTT TTTNCCTTTT	AAGAAAGCTT CTTGTGATG	CC 2104
TTNGGGGCTT	CTGTGAAAAA CCTGA	TGCAG TGCTCCATCC	AAACTCAGAA GGCTTTGG	GA 2164
TATGCTGTAT	TTTAAAGGGA CAGTT	TGTAA CTTGGGCTGT	AAAGCAAACT GGGGCTGT	GT 2224
TTTCGATGAT	GATGATNATC ATGAT	NATGA TNNNNNNNN	NNNNNNNN NNNNNNNN	NN 2284
NNNNNNNNN	GATTTTAACA GTTTT	ACTTC TGGCCTTTCC	TAGCTAGAGA AGGAGTTA	AT 2344
ATTTCTAAGG	TAACTCCCAT ATCTC	CTTTA ATGACATTGA	TTTCTAATGA TATAAATT	rc 2404
AGCCTACATT	GATGCCAAGC TTTTT	TGCCA CAAAGAAGAT	TCTTACCAAG AGTGGGCT	гт 2464
GTGGAAACAG	CTGGTACTGA TGTTC	ACCTT TATATATGTA	CTAGCATTTT CCACGCTG	AT 2524
GTTTATGTAC	TGTAAACAGT TCTGC	ACTCT TGTACAAAAG	AAAA	2568
	TION FOR SEQ ID			
(i)	SEQUENCE CHARACT (A) LENGTH: 46 (B) TYPE: amin (D) TOPOLOGY:	5 amino acids o acid		
(ii)	MOLECULE TYPE: p	rotein		
(xi)	SEQUENCE DESCRIP	TION: SEQ ID NO:2	2:	
		Phe Ala Leu Pro 10	Leu Leu Asp Leu Leu 15	
Leu Ser Ala	Glu Val Ser Gly 20	Gly Asp Arg Leu 25	Asp Cys Val Lys Ala · 30	
Ser Asp Gln 35	Cys Leu Lys Glu	Gln Ser Cys Ser	Thr Lys Tyr Arg Thr 45	
Leu Arg Gln 50	Cys Val Ala Gly 55		Phe Ser Leu Ala Ser 60	
Gly Leu Glu 65	Ala Lys Asp Glu 70	Cys Arg Ser Ala 75	Met Glu Ala Leu Lys 80	

Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu 85 90 95

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln 135 Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys 185 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys 230 Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala 280 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala 395 Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu

445 435 440 Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr 460 455 Ser 465 (2) INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2138 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 302..1705 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: AGCTCGCTCT CCCGGGGCAG TGGTGTGGAT GCACCGGAGT TCGGGCGCTG GGCAAGTTGG 60 GTCGGAACTG AACCCCTGAA AGCGGGTCCG CCTCCCGCCC TCGCGCCCGC CCGGATCTGA 120 180 GTCGCTGGCG GCGGTGGGCG GCAGAGCGAC GGGGAGTCTG CTCTCACCCT GGATGGAGCT GAACTTTGAG TGGCCAGAGG AGCGCAGTCG CCCGGGGATC GCTGCACGCT GAGCTCTCTC 240 300 CCCGAGACCG GGCGGCGGT TTGGATTTTG GGGGGGCGGG GACCAGCTGC GCGGCGGCAC C ATG TTC CTA GCC ACT CTG TAC TTC GCG CTG CCA CTC CTG GAT TTG 346 Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu CTG ATG TCC GCC GAG GTG AGT GGT GGA GAC CGT CTG GAC TGT GTG AAA 394 Leu Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys GCC AGC GAT CAG TGC CTG AAG GAA CAG AGC TGC AGC ACC AAG TAC CGC Ala Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg 442 35 ACA CTA AGG CAG TGC GTG GCG GGC AAG GAA ACC AAC TTC AGC CTG ACA 490 Thr Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Thr 50 TCC GGC CTT GAG GCC AAG GAT GAG TGC CGT AGC GCC ATG GAG GCC TTG 538 Ser Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu AAG CAG AAG TCT CTG TAC AAC TGC CGC TGC AAG CGG GGC ATG AAG AAA 586 Lys Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys

GAG AAG AAT TGT CTG CGT ATC TAC TGG AGC ATG TAC CAG AGC CTG CAG

Glu Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln

100

105

634

GGA Gly	AAT Asn	GAC Asp	CTC Leu 115	CTG Leu	GAA Glu	GAT Asp	TCC Ser	CCG Pro 120	TAT Tyr	GAG Glu	CCG Pro	GTT Val	AAC Asn 125	AGC Ser	AGG Arg	682
TTG Leu	TCA Ser	GAT Asp 130	ATA Ile	TTC Phe	CGG Arg	GCA Ala	GTC Val 135	CCG Pro	TTC Phe	ATA Ile	TCA Ser	GAT Asp 140	GTT Val	TTC Phe	CAG Gln	730
CAA Gln	GTG Val 145	GAA Glu	CAC His	ATT Ile	TCC Ser	AAA Lys 150	GGG Gly	AAC Asn	AAC Asn	TGC Cys	CTG Leu 155	GAC Asp	GCA Ala	GCC Ala	AAG Lys	778
GCC Ala 160	TGC Cys	AAC Asn	CTG Leu	GAC Asp	GAC Asp 165	ACC Thr	TGT Cys	AAG Lys	AAG Lys	TAC Tyr 170	AGG Arg	TCG Ser	GCC Ala	TAC Tyr	ATC Ile 175	826
ACC Thr	CCC Pro	TGC Cys	ACC Thr	ACC Thr 180	AGC Ser	ATG Met	TCC Ser	AAC Asn	GAG Glu 185	GTC Val	TGC Cys	AAC Asn	CGC Arg	CGT Arg 190	AAG Lys	874
TGC Cys	CAC His	AAG Lys	GCC Ala 195	CTC Leu	AGG Arg	CAG Gln	TTC Phe	TTC Phe 200	GAC Asp	AAG Lys	GTT Val	CCG Pro	GCC Ala 205	AAG Lys	CAC His	922
AGC Ser	TAC Tyr	GGG Gly 210	ATG Met	CTC Leu	TTC Phe	TGC Cys	TCC Ser 215	TGC Cys	CGG Arg	GAC Asp	ATC Ile	GCC Ala 220	TGC Cys	ACC Thr	GAG Glu	970
CGG Arg	CGG Arg 225	CGA Arg	CAG Gln	ACT Thr	ATC Ile	GTC Val 230	CCC Pro	GTG Val	TGC Cys	TCC Ser	TAT Tyr 235	GAA Glu	GAA Glu	CGA Arg	GAG Glu	1018
AGG Arg 240	CCC Pro	AAC Asn	TGC Cys	CTG Leu	AGT Ser 245	CTG Leu	CAA Gln	GAC Asp	TCC Ser	TGC Cys 250	AAG Lys	ACC Thr	AAT Asn	TAC Tyr	ATC Ile 255	1066
TGC Cys	AGA Arg	TCT Ser	CGC Arg	CTT Leu 260	GCA Ala	GAT Asp	TTT Phe	TTT Phe	ACC Thr 265	AAC Asn	TGC Cys	CAG Gln	CCA Pro	GAG Glu 270	TCA Ser	1114
AGG Arg	TCT Ser	GTC Val	AGC Ser 275	AAC Asn	TGT Cys	CTT Leu	AAG Lys	GAG Glu 280	AAC Asn	TAC Tyr	GCA Ala	GAC Asp	TGC Cys 285	CTC Leu	CTG Leu	1162
GCC Ala	TAC Tyr	TCG Ser 290	GGA Gly	CTG Leu	ATT Ile	GGC Gly	ACA Thr 295	GTC Val	ATG Met	ACT Thr	CCC Pro	AAC Asn 300	TAC Tyr	GTA Val	GAC Asp	1210
TCC Ser	AGC Ser 305	AGC Ser	CTC Leu	AGC Ser	GTG Val	GCA Ala 310	CCA Pro	TGG Trp	TGT Cys	GAC Asp	TGC Cys 315	AGC Ser	AAC Asn	AGC Ser	GGC Gly	1258
AAT Asn 320	GAC Asp	CTG Leu	GAA Glu	GAC Asp	TGC Cys 325	TTG Leu	AAA Lys	TTT Phe	CTG Leu	AAT Asn 330	TTT Phe	TTT Phe	AAG Lys	GAC Asp	AAT Asn 335	1306
ACT Thr	TGT Cys	CTC Leu	AAA Lys	AAT Asn 340	GCA Ala	ATT Ile	CAA Gln	GCC Ala	TTT Phe 345	GGC Gly	AAT Asn	GGC Gly	TCA Ser	GAT Asp 350	GTG Val	1354
ACC Thr	ATG Met	TGG Trp	CAG Gln 355	CCA Pro	GCC Ala	CCT Pro	CCA Pro	GTC Val 360	CAG Gln	ACC Thr	ACC Thr	ACT Thr	GCC Ala 365	ACC Thr	ACT Thr	1402

ACC Thr	ACT Thr	GCC Ala 370	TTC Phe	CGG Arg	GTC Val	AAG Lys	AAC Asn 375	AAG Lys	CCT Pro	CTG Leu	GGG Gly	CCA Pro 380	GCA Ala	GGG Gly	TCT Ser	145	5 C
GAG Glu	AAT Asn 385	GAG Glu	ATC Ile	CCC Pro	ACA Thr	CAC His 390	GTT Val	TTA Leu	CCA Pro	CCC Pro	TGT Cys 395	GCG Ala	AAT Asn	TTG Leu	CAG Gln	149	9€
GCT Ala 400	CAG Gln	AAG Lys	CTG Leu	AAA Lys	TCC Ser 405	AAT Asn	GTG Val	TCG Ser	GGT Gly	AGC Ser 410	ACA Thr	CAC His	CTC Leu	TGT Cys	CTT Leu 415	154	16
TCT Ser	GAT Asp	AGT Ser	GAT Asp	TTC Phe 420	GGA Gly	AAG Lys	GAT Asp	GGT Gly	CTC Leu 425	GCT Ala	GGT Gly	GCC Ala	TCC Ser	AGC Ser 430	CAC His	159	€
ATA Ile	ACC Thr	ACA Thr	AAA Lys 435	TCA Ser	ATG Met	GCT Ala	GCT Ala	CCT Pro 440	CCC Pro	AGC Ser	TGC Cys	AGT Ser	CTG Leu 445	AGC Ser	TCA Ser	164	12
CTG Leu	CCG Pro	GTG Val 450	CTG Leu	ATG Met	CTC Leu	ACC Thr	GCC Ala 455	CTT Leu	GCT Ala	GCC Ala	CTG Leu	TTA Leu 460	TCT Ser	GTA Val	TCG Ser	169	90
			ACG Thr		TAGO	CTGC#	ATC C	CGGGI	AAAC	CA GT	PATG#	\AAA(AC	AAAA(GAGA	174	15
ACC	AGTA	ATT C	CTGTC	CCTC	T CO	CTCTI	GTAI	TA T	TGA	TAA	CCAC	FTTTT	raa A	AAGCT	CCGTT	180	05
GAG	AGCA	AGT T	TCAC	CCAZ	AC TO	GAAC	CTCTI	TCC	CTTGT	$\mathbf{T}\mathbf{T}\mathbf{T}$	TAAC	SAAAC	GCT T	rgtgo	SCCCTC	186	55
AGGG	GCTT	CT C	STTGA	AGAZ	AC TO	CTAC	CAGGO	G CTA	ATTO	CAA	ACCO	CATAZ	AGG (CTCTC	GGGCG	192	25
TGGI	GCGG	CT T	raago	GGAC	CC AT	rTTGC	CACCA	A TGT	'AAA'	CAA	GCT	GGCT	TA T	CATO	STGTTT	198	35
GATO	GTGA	AGG A	ATGGT	PAGTO	G TO	SATGA	TGAT	r GG1	TAATI	ATT	ACAG	CTTC	SAA (ССТС	STTCTC	204	45
TCTA	CTGG	TT A	AGGAA	CAGG	SA GA	TACI	TATT	ATA	AAGA	ATTC	TTCC	CATGI	rc r 1	гасто	CAGCAG	210	05
CATI	GCCI	TC T	rgaac	BACAC	G C	CCGC	AGCCG	TCC	}							213	38

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 468 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu 1 5 10 15

Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala 20 25 30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr 35 40 45

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Thr Ser

55 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu 85 90 . 95 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu Ser Asp Ile Phe Arg Ala Val Pro Phe Ile Ser Asp Val Phe Gln Gln Val Glu His Ile Ser Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp Thr Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr 165 170 175 Pro Cys Thr Thr Ser Met Ser Asn Glu Val Cys Asn Arg Arg Lys Cys 185 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser 200 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Arg 225 230 235 230 Pro Asn Cys Leu Ser Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Asn Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala 280 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Val Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr 330 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Met Trp Gln Pro Ala Pro Pro Val Gln Thr Thr Ala Thr Thr Thr Thr Ala Phe Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu 380 375 Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala

Gln	Lys	Leu	Lys	Ser 405		Val	Ser	Gly	Ser 410	Thr	His	Leu	Cys	Leu 415	Ser
Asp	Ser	Asp		Gly			Gly	Leu 425	Ala	Gly	Ala	Ser	Ser 430	His	Ile
Thr	Thr	Lys	Ser	Met	Ala	Ala	Pro	Pro	Ser	Cys	Ser	Leu	Ser	Ser	Leu

435 440 445

Pro Val Leu Met Leu Thr Ala Leu Ala Ala Leu Leu Ser Val Ser Leu 460 455 450

Ala Glu Thr Ser 465

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature (B) LOCATION: 1..539
- (D) OTHER INFORMATION: /note= "1 to 539 is -237 to 301 of Figure 5 Gdnfr"
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 540..1937
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AATCTGGCCT CGGAAC	CACGC CATTCTCCGC	GCCGCTTCCA	ATAACCACTA	ACATCCCTAA	60
CGAGCATCCG AGCCGA	AGGGC TCTGCTCGGA	AATCGTCCTG	GCCCAACTCG	GCCCTTCGAG	120
CTCTCGAAGA TTACCG	CATC TATTTTTTT	TTCTTTTTT	TCTTTTCCTA	GCGCAGATAA	180
AGTGAGCCCG GAAAGG	GAAG GAGGGGGCGG	GGACACCATT	GCCCTGAAAG	AATAAATAAG	240
TAAATAAACA AACTGG	GCTCC TCGCCGCAGC	TGGACGCGGT	CGGTTGAGTC	CAGGTTGGGT	300
CGGACCTGAA CCCCTA	AAAAG CGGAACCGCC	TCCCGCCCTC	GCCATCCCGG	AGCTGAGTCG	360
CCGGCGGCGG TGGCTG	GCTGC CAGACCCGGA	GTTTCCTCTT	TCACTGGATG	GAGCTGAACT	420
TTGGGCGGCC AGAGCA	AGCAC AGCTGTCCGG	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCAA	480
GACCCAGCGG CGGCTC	GGGA TTTTTTTGGG	GGGGCGGGA	CCAGCCCCGC	GCCGGCACC	539
ATG TTC CTG GCG A Met Phe Leu Ala T 1	ACC CTG TAC TTC C Thr Leu Tyr Phe 7 5	GCG CTG CCG Ala Leu Pro 10	CTC TTG GAC Leu Leu Asp	C TTG CTC Leu Leu 15	587
CTG TCG GCC GAA G Leu Ser Ala Glu V	GTG AGC GGC GGA (GAC CGC CTG Asp Arg Leu	GAT TGC GTC Asp Cys Val	G AAA GCC L Lys Ala	635

			20					25					30			
AGT (GAT Asp	CAG Gln 35	TGC Cys	CTG Leu	AAG Lys	GAG Glu	CAG Gln 40	AGC Ser	TGC Cys	AGC Ser	ACC Thr	AAG Lys 45	TAC Tyr	CGC Arg	ACG Thr	683
CTA . Leu .	AGG Arg 50	CAG Gln	TGC Cys	GTG Val	GCG Ala	GGC Gly 55	AAG Lys	GAG Glu	ACC Thr	AAC Asn	TTC Phe 60	AGC Ser	CTG Leu	GCA Ala	TCC Ser	731
GGC Gly 65	CTG Leu	GAG Glu	GCC Ala	AAG Lys	GAT Asp 70	GAG Glu	TGC Cys	CGC Arg	AGC Ser	GCC Ala 75	ATG Met	GAG Glu	GCC Ala	CTG Leu	AAG Lys 80	779
CAG Gln	AAG Lys	TCG Ser	CTC Leu	TAC Tyr 85	AAC Asn	TGC Cys	CGC Arg	TGC Cys	AAG Lys 90	CGG Arg	GGT Gly	ATG Met	AAG Lys	AAG Lys 95	GAG Glu	827
AAG . Lys .	AAC Asn	TGC Cys	CTG Leu 100	CGC Arg	ATT Ile	TAC Tyr	TGG Trp	AGC Ser 105	ATG Met	TAC Tyr	CAG Gln	AGC Ser	CTG Leu 110	CAG Gln	GGA Gly	875
AAT Asn	GAT Asp	CTG Leu 115	CTG Leu	GAG Glu	GAT Asp	TCC Ser	CCA Pro 120	TAT Tyr	GAA Glu	CCA Pro	GTT Val	AAC Asn 125	AGC Ser	AGA Arg	TTG Leu	923
TCA Ser	GAT Asp 130	ATA Ile	TTC Phe	CGG Arg	GTG Val	GTC Val 135	CCA Pro	TTC Phe	ATA Ile	TCA Ser	GAT Asp 140	GTT Val	TTT Phe	CAG Gln	CAA Gln	971
GTG Val 145	GAG Glu	CAC His	ATT Ile	CCC Pro	AAA Lys 150	GGG Gly	AAC Asn	AAC Asn	TGC Cys	CTG Leu 155	GAT Asp	GCA Ala	GCG Ala	AAG Lys	GCC Ala 160	1019
TGC . Cys .	AAC Asn	CTC Leu	GAC Asp	GAC Asp 165	ATT Ile	TGC Cys	AAG Lys	AAG Lys	TAC Tyr 170	AGG Arg	TCG Ser	GCG Ala	TAC Tyr	ATC Ile 175	ACC Thr	1067
CCG Pro	TGC Cys	ACC Thr	ACC Thr 180	AGC Ser	GTG Val	TCC Ser	AAN Xaa	GAT Asp 185	GTC Val	TGC Cys	AAC Asn	CGC Arg	CGC Arg 190	AAG Lys	TGC Cys	1115
CAC His	AAG Lys	GCC Ala 195	CTC Leu	CGG Arg	CAG Gln	TTC Phe	TTT Phe 200	GAC Asp	AAG Lys	GTC Val	CCG Pro	GCC Ala 205	AAG Lys	CAC His	AGC Ser	1163
TAC Tyr	GGA Gly 210	ATG Met	CTC Leu	TTC Phe	TGC Cys	TCC Ser 215	TGC Cys	CGG Arg	GAC Asp	ATC Ile	GCC Ala 220	TGC Cys	ACA Thr	GAG Glu	CGG Arg	1211
AGG Arg 225	CGA Arg	CAG Gln	ACC Thr	ATC Ile	GTG Val 230	CCT Pro	GTG Val	TGC Cys	TCC Ser	TAT Tyr 235	GAA Glu	GAG Glu	AGG Arg	GAG Glu	AAG Lys 240	1259
CCC Pro	AAC Asn	TGT Cys	TTG Leu	AAT Asn 245	TTG Leu	CAG Gln	GAC Asp	TCC Ser	TGC Cys 250	AAG Lys	ACG Thr	AAT Asn	TAC Tyr	ATC Ile 255	TGC Cys	1307
AGA Arg	TCT Ser	CGC Arg	CTT Leu 260	GCG Ala	GAT Asp	TTT Phe	TTT Phe	ACC Thr 265	AAC Asn	TGC Cys	CAG Gln	CCA Pro	GAG Glu 270	TCA Ser	AGG Arg	1355
TCT Ser	GTC Val	AGC Ser	AGC Ser	TGT Cys	CTA Leu	AAG Lys	GAA Glu	AAC Asn	TAC Tyr	GCT Ala	GAC Asp	TGC Cys	CTC Leu	CTC Leu	GCC Ala	1403

275		280	2	185	
TAC TCG GGG CTT Tyr Ser Gly Leu 290					
AGT AGC CTC AGT Ser Ser Leu Ser 305	GTG GCC CCA Val Ala Pro 310	TGG TGT GAC Trp Cys Asp	TGC AGC A Cys Ser A 315	AAC AGT GGG Asn Ser Gly	AAC 1499 Asn 320
GAC CTA GAA GAG Asp Leu Glu Glu	TGC TTG AAA Cys Leu Lys 325	TTT TTG AAT Phe Leu Asn 330	Phe Phe L	AAG GAC AAT Lys Asp Asn 335	ACA 1547 Thr
TGT CTT AAA AAT Cys Leu Lys Asn 340	Ala Ile Gln	GCC TTT GGC Ala Phe Gly 345	AAT GGC T Asn Gly S	CCC GAT GTG Ser Asp Val 350	ACC 1595 Thr
GTG TGG CAG CCA Val Trp Gln Pro 355	GCC TTC CCA Ala Phe Pro	GTA CAG ACC Val Gln Thr 360	Thr Thr A	GCC ACT ACC Ala Thr Thr 165	ACC 1643 Thr
ACT GCC CTC CGG Thr Ala Leu Arg 370	GTT AAG AAC Val Lys Asn 375	AAG CCC CTG Lys Pro Leu	GGG CCA G Gly Pro A 380	GCA GGG TCT Ala Gly Ser	GAG 1691 Glu
AAT GAA ATT CCC Asn Glu Ile Pro 385	ACT CAT GTT Thr His Val 390	TTG CCA CCG Leu Pro Pro	TGT GCA A Cys Ala A 395	AT TTA CAG Asn Leu Gln	GCA 1739 Ala 400
CAG AAG CTG AAA Gln Lys Leu Lys	TCC AAT GTG Ser Asn Val 405	TCG GGC AAT Ser Gly Asn 410	Thr His L	TC TGT ATT Leu Cys Ile 415	TCC 1787 Ser
AAT GGT AAT TAT Asn Gly Asn Tyr 420	GAA AAA GAA Glu Lys Glu	GGT CTC GGT Gly Leu Gly 425	GCT TCC A Ala Ser S	AGC CAC ATA Ser His Ile 430	ACC 1835 Thr
ACA AAA TCA ATG Thr Lys Ser Met 435	GCT GCT CCT Ala Ala Pro	CCA AGC TGT Pro Ser Cys 440	Gly Leu S	AGC CCA CTG Ser Pro Leu .45	CTG 1883 Leu
GTC CTG GTG GTA Val Leu Val Val 450	ACC GCT CTG Thr Ala Leu 455	TCC ACC CTA Ser Thr Leu	TTA TCT T Leu Ser L 460	TTA ACA GAA eu Thr Glu	ACA 1931 Thr
TCA TAG CTGCATT Ser * 465	AAA AAAATACAA	AT ATGGACATG	т ааааадас	AA AAACCAA	GTT 1987
ATCTGTTTCC TGTT	CTCTTG TATAGO	CTGAA ATTCCA	GTTT AGGAG	CTCAG TTGA	GAAACA 2047
GTTCCATTCA ACTG	GAACAT TTTTT	TTTTT NCCTTT	TAAG AAAGC	TTCTT GTGA	TCCTTC 2107
GGGGCTTCTG TGAA	AAACCT GATGCA	AGTGC TCCATC	CAAA CTCAG	AAGGC TTTG	GGATAT 2167
GCTGTATTTT AAAG	GGACAG TTTGTA	AACTT GGGCTG	тааа ссааа	CTGGG GCTG	TGTTTT 2227
CGATGATGAT GATC	ATCATG ATCATO	GATNN NNNNN	NNNN NNNN	INNNNN NNNN	NNNNNN 2287
NNNNNNNGAT TTTA	ACAGTT TTACTT	CTGG CCTTTC	CTAG CTAGA	GAAGG AGTT	AATATT 2347
TCTAAGGTAA CTCC	CATATC TCCTTT	TAATG ACATTG	АТТТ СТААТ	GATAT AAAT	TTCAGC 2407

CTACATTGAT	GCCAAGCTTT	TTTGCCACAA	AGAAGATTCT	TACCAAGAGT	GGGCTTTGTG	2467
GAAACAGCTG	GTACTGATGT	TCACCTTTAT	ATATGTACTA	GCATTTTCCA	CGCTGATGTT	2527
TATGTACTGT	AAACAGTTCT	GCACTCTTGT	ACAAAAGAAA	AAACACCTGT	CACATCCAAA	2587
TATAGTATCT	GTCTTTTCGT	CAAAATAGAG	AGTGGGGAAT	GAGTGTGCCG	ATTCAATACC	2647
TCAATCCCTG	AACGACACTC	TCCTAATCCT	AAGCCTTACC	TGAGTGAGAA	GCCCTTTACC	2707
TAACAAAAGT	CCAATATAGC	TGAAATGTCG	CTCTAATACT	CTTTACACAT	ATGAGGTTAT	2767
ATGTAGAAAA	AAATTTTACT	ACTAAATGAT	TTCAACTATT	GGCTTTCTAT	ATTTTGAAAG	2827
TAATGATATT	GTCTCATTTT	TTTACTGATG	GTTTAATACA	AAATACACAG	AGCTTGTTTC	2887
CCCTCATAAG	TAGTGTTCGC	TCTGATATGA	ACTTCACAAA	TACAGCTCAT	CAAAAGCAGA	2947
CTCTGAGAAG	CCTCGTGCTG	TAGCAGAAAG	TTCTGCATCA	TGTGACTGTG	GACAGGCAGG	3007
AGGAAACAGA	ACAGACAAGC	ATTGTCTTTT	GTCATTGCTC	GAAGTGCAAG	CGTGCATACC	3067
TGTGGAGGGA	ACTGGTGGCT	GCTTGTAAAT	GTTCTGCAGC	ATCTCTTGAC	ACACTTGTCA	3127
TGACACAATC	CAGTACCTTG	GTTTTCAGGT	TATCTGACAA	AGGCAGCTTT	GATTGGGACA	3187
TGGAGGCATG	GGCAGGCCGG	AA				3209

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 466 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu 10 Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser 50 55 60 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys 65 70 75 80 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu 85 90 95 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly 100 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu

120

Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr 170 165 Pro Cys Thr Thr Ser Val Ser Xaa Asp Val Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser 200 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg 215 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg 260 Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala 280 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn 315 Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr 330 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr 360 Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu 375 Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala 385 400 390 Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser 410 Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu 440 Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr

Ser *

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..508
 (D) OTHER INFORMATION: /note= "1 to 508 is -237 to 272 of Figure 5 Hsgr-21af"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCTGGCCTCG	GAACACGCCA	TTCTCCGCGC	CGCTTCCAAT	AACCACTAAC	ATCCCTAACG	60
AGCATCCGAG	CCGAGGGCTC	TGCTCGGAAA	TCGTCCTGGC	CCAACTCGGC	CCTTCGAGCT	120
CTCGAAGATT	ACCGCATCTA	TTTTTTTTT	CTTTTTTTC	TTTTCCTAGC	GCAGATAAAG	180
TGAGCCCGGA	AAGGGAAGGA	GGGGGGGGG	ACACCATTGC	CCTGAAAGAA	TAAATAAGTA	240
ААТАААСААА	CTGGCTCCTC	GCCGCAGCTG	GACGCGGTCG	GTTGAGTCCA	GGTTGGGTCG	300
GACCTGAACC	CCTAAAAGCG	GAACCGCCTC	CCGCCCTCGC	CATCCCGGAG	CTGAGTCGCC	360
GGCGGCGGTG	GCTGCTGCCA	GACCCGGAGT	TTCCTCTTTC	ACTGGATGGA	GCTGAACTTT	420
GGGCGGCCAG	AGCAGCACAG	CTGTCCGGGG	ATCGCTGCAC	GCTGAGCTCC	CTCGGCAAGA	480
CCCAGCGGCG	GCTCGGGATT	TTTTTGGG				508

- (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 510 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..510
 - (D) OTHER INFORMATION: /note= "1 to 510 is -237 to 272 of Figure 5 Hsgr-21bf"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
- 60 AATCTGGCCT CGGAACACGC CATTCTCCGC GCCGCTTCCA ATAACCACTA ACATCCCTAA CGAGCATCCG AGCCGAGGGC TCTGCTCGGA AATCGTCCTG GCCCAACTCG GCCCTTCGAG 120

CTCTCGAAGA	TTACCGCATC	$\mathbf{TATTTTTTTT}$	${\bf TTCTTTTTT}$	TCTTTTCCTA	GCGCAGATAA	180
AGTGAGCCCG	GAAAGGGAAG	GAGGGGGCGG	GGACACCATT	GCCCTGAAAG	AATAAATAAG	240
ТАААТАААСА	AACTGGCTCC	TCGCCGCAGC	TGGACGCGGT	CGGTTGAGTC	CAGGTTGGGT	300
CGGACCTGAA	CCCCTAAAAG	CGGAACCGCC	TCCCGCCCTC	GCCATCCCGG	AGCTGAGTCG	360
ccgccgccg	TGGCTGCTGC	CAGACCCGGA	GTTTCCTCTT	TCACTGGATG	GAGCTGAACT	420
TTGGGCGGCC	AGAGCAGCAC	AGCTGTCCGG	GGATCGCTGC	ACGCTGAGCT	CCCTCGGCAA	480
GACCCAGCGG	CGGCTCGGGA	TTTTTTTGGG				510

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1927 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

 - (A) NAME/KEY: CDS
 (B) LOCATION: 538..1926
- (ix) FEATURE:
- (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..537
 (D) OTHER INFORMATION: /note= "1 to 537 is -235 to 301 of Figure 5 21acon"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCTGGCCTCG GAACACGCCA TTCTCCGCGC CGCTTCCAAT AACCACTAAC ATCCCTAACG	60
AGCATCCGAG CCGAGGGCTC TGCTCGGAAA TCGTCCTGGC CCAACTCGGC CCTTCGAGCT	120
CTCGAAGATT ACCGCATCTA TTTTTTTTT CTTTTTTTC TTTTCCTAGC GCAGATAAAG	180
TGAGCCCGGA AAGGGAAGGA GGGGGCGGGG ACACCATTGC CCTGAAAGAA TAAATAAGTA	240
AATAAACAAA CTGGCTCCTC GCCGCAGCTG GACGCGGTCG GTTGAGTCCA GGTTGGGTCG	300
GACCTGAACC CCTAAAAGCG GAACCGCCTC CCGCCCTCGC CATCCCGGAG CTGAGTCGCC	360
GGCGGCGGTG GCTGCTGCCA GACCCGGAGT TTCCTCTTTC ACTGGATGGA GCTGAACTTT	420
GGGCGGCCAG AGCAGCACAG CTGTCCGGGG ATCGCTGCAC GCTGAGCTCC CTCGGCAAGA	480
CCCAGCGGCG GCTCGGGATT TTTTTGGGGG GGCGGGGACC AGCCCCGCGC CGGCACC	537
ATG TTC CTG GCG NCC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC Met Phe Leu Ala Xaa Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu 1 5 10	585
CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala 20 25 30	633

AGT Ser	GAT Asp	CAG Gln 35	TGC Cys	CTG Leu	AAG Lys	GAG Glu	CAG Gln 40	AGC Ser	TGC Cys	AGC Ser	ACC Thr	AAG Lys 45	TAC Tyr	CGC Arg	ACG Thr	681
CTA Leu	AGG Arg 50	CAG Gln	TGC Cys	GTG Val	GCG Ala	GGC Gly 55	AAG Lys	GAG Glu	ACC Thr	AAC Asn	TTC Phe 60	AGC Ser	CTG Leu	GCA Ala	TCC Ser	729
GGC Gly 65	CTG Leu	GAG Glu	GCC Ala	AAG Lys	GAT Asp 70	GAG Glu	TGC Cys	CGC Arg	AGC Ser	GCC Ala 75	ATG Met	GAG Glu	GCC Ala	CTG Leu	AAG Lys 80	777
CAG Gln	AAG Lys	TCG Ser	CTC Leu	TAC Tyr 85	AAC Asn	TGC Cys	CGC Arg	TGC Cys	AAG Lys 90	CGG Arg	GGT Gly	ATG Met	AAG Lys	AAG Lys 95	GAG Glu	825
AAG Lys	AAC Asn	TGC Cys	CTG Leu 100	CGC Arg	ATT Ile	TAC Tyr	TGG Trp	AGC Ser 105	ATG Met	TAC Tyr	CAG Gln	AGC Ser	CTG Leu 110	CAG Gln	GGA Gly	873
AAT Asn	GAT Asp	CTG Leu 115	CTG Leu	GAG Glu	GAT Asp	TCC Ser	CCA Pro 120	TAT Tyr	GAA Glu	CCA Pro	GTT Val	AAC Asn 125	AGC Ser	AGA Arg	TTG Leu	921
TCA Ser	GAT Asp 130	ATA Ile	TTC Phe	CGG Arg	GTG Val	GTC Val 135	CCA Pro	TTC Phe	ATA Ile	TCA Ser	GAT Asp 140	GTT Val	TTT Phe	CAG Gln	CAA Gln	969
GTG Val 145	GAG Glu	CAC His	ATT Ile	CCC Pro	AAA Lys 150	GGG Gly	AAC Asn	AAC Asn	TGC Cys	CTG Leu 155	GAT Asp	GCA Ala	GCG Ala	AAG Lys	GCC Ala 160	1017
TGC Cys	AAC Asn	CTC Leu	GAC Asp	GAC Asp 165	ATT Ile	TGC Cys	AAG Lys	AAG Lys	TAC Tyr 170	AGG Arg	TCG Ser	GCG Ala	TAC Tyr	ATC Ile 175	ACC Thr	1065
CCG Pro	TGC Cys	ACC Thr	ACC Thr 180	AGC Ser	GTG Val	TCC Ser	AAC Asn	GAT Asp 185	GTC Val	TGC Cys	AAC Asn	CGC Arg	CGC Arg 190	AAG Lys	TGC Cys	1113
CAC His	AAG Lys	GCC Ala 195	CTC Leu	CGG Arg	CAG Gln	TTC Phe	TTT Phe 200	GAC Asp	AAG Lys	GTC Val	CCG Pro	GCC Ala 205	AAG Lys	CAC His	AGC Ser	1161
TAC Tyr	GGA Gly 210	ATG Met	CTC Leu	TTC Phe	TGC Cys	TCC Ser 215	TGC Cys	CGG Arg	GAC Asp	ATC Ile	GCC Ala 220	TGC Cys	ACA Thr	GAG Glu	CGG Arg	1209
AGG Arg 225	CGA Arg	CAG Gln	ACC Thr	ATC Ile	GTG Val 230	CCT Pro	GTG Val	TGC Cys	TCC Ser	TAT Tyr 235	GAA Glu	GAG Glu	AGG Arg	GAG Glu	AAG Lys 240	1257
CCC Pro	AAC Asn	TGT Cys	TTG Leu	AAT Asn 245	TTG Leu	CAG Gln	GAC Asp	TCC Ser	TGC Cys 250	AAG Lys	ACG Thr	AAT Asn	TAC Tyr	ATC Ile 255	TGC Cys	1305
AGA Arg	TCT Ser	CGC Arg	CTT Leu 260	GCG Ala	GAT Asp	TTT Phe	TTT Phe	ACC Thr 265	AAC Asn	TGC Cys	CAG Gln	CCA Pro	GAG Glu 270	TCA Ser	AGG Arg	1353
TCT Ser	GTC Val	AGC Ser 275	AGC Ser	TGT Cys	CTA Leu	AAG Lys	GAA Glu 280	AAC Asn	TAC Tyr	GCT Ala	GAC Asp	TGC Cys 285	CTC Leu	CTC Leu	GCC Ala	1401

TAC Tyr	TCG Ser 290	GGG Gly	CTT Leu	ATT Ile	GGC Gly	ACA Thr 295	GTC Val	ATG Met	ACC Thr	CCC Pro	AAC Asn 300	TAC Tyr	ATA Ile	GAC Asp	TCC Ser	1449
AGT Ser 305	AGC Ser	CTC Leu	AGT Ser	GTG Val	GCC Ala 310	CCA Pro	TGG Trp	TGT Cys	GAC Asp	TGC Cys 315	AGC Ser	AAC Asn	AGT Ser	GGG Gly	AAC Asn 320	1497
GAC Asp	CTA Leu	GAA Glu	GAG Glu	TGC Cys 325	TTG Leu	AAA Lys	TTT Phe	TTG Leu	AAT Asn 330	TTC Phe	TTC Phe	AAG Lys	GAC Asp	AAT Asn 335	ACA Thr	1545
TGT Cys	CTT Leu	AAA Lys	AAT Asn 340	GCA Ala	ATT Ile	CAA Gln	GCC Ala	TTT Phe 345	GGC Gly	AAT Asn	GGC Gly	TCC Ser	GAT Asp 350	GTG Val	ACC Thr	1593
GTG Val	TGG Trp	CAG Gln 355	CCA Pro	GCC Ala	TTC Phe	CCA Pro	GTA Val 360	CAG Gln	ACC Thr	ACC Thr	ACT Thr	GCC Ala 365	ACT Thr	ACC Thr	ACC Thr	1641
ACT Thr	GCC Ala 370	CTC Leu	CGG Arg	GTT Val	AAG Lys	AAC Asn 375	AAG Lys	CCC Pro	CTG Leu	GGG Gly	CCA Pro 380	GCA Ala	GGG Gly	TCT Ser	GAG Glu	1689
AAT Asn 385	GAA Glu	ATT Ile	CCC Pro	ACT Thr	CAT His 390	GTT Val	TTG Leu	CCA Pro	CCG Pro	TGT Cys 395	GCA Ala	AAT Asn	TTA Leu	CAG Gln	GCA Ala 400	1737
CAG Gln	AAG Lys	CTG Leu	AAA Lys	TCC Ser 405	AAT Asn	GTG Val	TCG Ser	GGC Gly	AAT Asn 410	ACA Thr	CAC His	CTC Leu	TGT Cys	ATT Ile 415	TCC Ser	1785
AAT Asn	GGT Gly	AAT Asn	TAT Tyr 420	GAA Glu	AAA Lys	GAA Glu	GGT Gly	CTC Leu 425	GGT Gly	GCT Ala	TCC Ser	AGC Ser	CAC His 430	ATA Ile	ACC Thr	1833
ACA Thr	AAA Lys	TCA Ser 435	ATG Met	GCT Ala	GCT Ala	CCT Pro	CCA Pro 440	AGC Ser	TGT Cys	GGT Gly	CTG Leu	AGC Ser 445	CCA Pro	CTG Leu	CTG Leu	1881
GTC Val	CTG Leu 450	GTG Val	GTA Val	ACC Thr	GCT Ala	CTG Leu 455	TCC Ser	ACC Thr	CTA Leu	TTA Leu	TCT Ser 460	TTA Leu	ACA Thr	GAA Glu		1926
A																1927

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Phe Leu Ala Xaa Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu 1 5 10 15

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala 20 25 30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
70 75 80 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu 120 Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr 165 Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser 200 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg 215 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys 225 230 235 240 Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala 280 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr 330 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu

	370					375					380					
Asn 385	Glu	Ile	Pro	Thr	His 390	Val	Leu	Pro	Pro	Cys 395	Ala	Asn	Leu	Gln	Ala 400	
Gln	Lys	Leu	Lys	Ser 405	Asn	Val	Ser	Gly	Asn 410	Thr	His	Leu	Cys	Ile 415	Ser	
Asn	Gly	Asn	Tyr 420	Glu	Lys	Glu	Gly	Leu 425	Gly	Ala	Ser	Ser	His 430	Ile	Thr	
Thr	Lys	Ser 435	Met	Ala	Ala	Pro	Pro 440	Ser	Cys	Gly	Leu	Ser 445	Pro	Leu	Leu	
Val	Leu 450	Val	Val	Thr	Ala	Leu 455	Ser	Thr	Leu	Leu	Ser 460	Leu	Thr	Glu	-	
(2)	INFO	ORMA	rion	FOR	SEQ	ID 1	10:13	l :								
		(I (I (I	QUENCA) LI B) TY C) SY O) TO	ENGTH PE: PRANI	H: 19 nucl DEDNI DGY:	29 h Leic ESS: line	ase acio sino ear	pai:	cs							
	(ii)	MOI	LECUI	LE TY	PE:	cDNA	A									
	(ix)	(2	ATURI A) NA B) LO	ME/I			192	28								
Fi		() (I (I	ATURI A) NA B) L(D) OT 21bc	AME/I CAT: THER	ON:	15	539			"1 t	to 53	39 is	s -2:	37 to	301 of	
	(xi)	SE	QUENC	CE DI	ESCRI	PTIC	on: s	SEQ I	D NO):11:	:					
AATO	CTGGC	CCT (CGGA	ACAC	GC CA	ATTCI	rccgo	C GCC	CGCTI	CCA	ATA	ACCA	CTA A	ACATO	CCTAA	60
CGAC	CATO	CCG A	AGCC	GAGG	C TO	CTGCT	rcggz	AA AA	CGTO	CTG	GCC	CAAC	rcg (GCCC	TTCGAG	120
CTCT	CGA	AGA 1	rtac(GCA	C T	TTT	r TT T:	г тто	CTTTI	TTTT	TCTT	TTTC	CTA (GCGC?	AGATAA	180
AGTO	SAGCO	CCG (SAAAC	GGA	AG GA	AGGGG	GCG	G GGA	ACACO	CATT	GCC	CTGA	AAG A	ATA	ATAAG	240
TAAA	AATA	ACA A	AACTO	GCT	CC TO	CGCC	GCAG	C TGC	GACGO	CGGT	CGG	TGA	TC (CAGG	TTGGGT	300
CGG	ACCTO	GAA (CCCC	TAAA1	AG CO	GAA	CCGC	TCC	CCGC	CCTC	GCCZ	ATCC	CGG Z	AGCT	GAGTCG	360
CCG	GCGG	CGG 7	rggc	rgcto	GC CA	GAC	CCGG	A GT	rtcci	гстт	TCAC	CTGG	ATG (GAGC	TGAACT	420
TTGO	GCG	GCC A	AGAG	CAGC	AC AC	CTG	rccg	G GGZ	ATCGO	CTGC	ACG	CTGA	GCT (CCCT	CGGCAA	480
GAC	CCAG	CGG (CGGC:	rcgg	GA T	TTTT	rtgg	G GGG	GCG	GGA	CCAC	CCC	CGC (GCCG	GCACC	539
ATG Met 1	TTC Phe	CTG Leu	GCG Ala	ACC Thr 5	CTG Leu	TAC Tyr	TTC Phe	GCG Ala	CTG Leu 10	CCG Pro	CTC Leu	TTG Leu	GAC Asp	TTG Leu 15	CTC Leu	587
CTG	TCG	GCC	GAA	GTG	AGC	GGC	GGA	GAC	CGC	CTG	GAT	TGC	GTG	AAA	GCC	635

Leu	Ser	Ala	Glu 20	Val	Ser	Gly	Gly	Asp 25	Arg	Leu	Asp	Cys	Val 30	Lys	Ala	
AGT Ser	GAT Asp	CAG Gln 35	TGC Cys	CTG Leu	AAG Lys	GAG Glu	CAG Gln 40	AGC Ser	TGC Cys	AGC Ser	ACC Thr	AAG Lys 45	TAC Tyr	CGC Arg	ACG Thr	683
CTA Leu	AGG Arg 50	CAG Gln	TGC Cys	GTG Val	GCG Ala	GGC Gly 55	AAG Lys	GAG Glu	ACC Thr	AAC Asn	TTC Phe 60	AGC Ser	CTG Leu	GCA Ala	TCC Ser	731
GGC Gly 65	CTG Leu	GAG Glu	GCC Ala	AAG Lys	GAT Asp 70	GAG Glu	TGC Cys	CGC Arg	AGC Ser	GCC Ala 75	ATG Met	GAG Glu	GCC Ala	CTG Leu	AAG Lys 80	779
CAG Gln	AAG Lys	TCG Ser	CTC Leu	TAC Tyr 85	AAC Asn	TGC Cys	CGC Arg	TGC Cys	AAG Lys 90	CGG Arg	GGT Gly	ATG Met	AAG Lys	AAG Lys 95	GAG Glu	827
AAG Lys	AAC Asn	TGC Cys	CTG Leu 100	CGC Arg	ATT Ile	TAC Tyr	TGG Trp	AGC Ser 105	ATG Met	TAC Tyr	CAG Gln	AGC Ser	CTG Leu 110	CAG Gln	GGA Gly	875
AAT Asn	GAT Asp	CTG Leu 115	CTG Leu	GAG Glu	GAT Asp	TCC Ser	CCA Pro 120	TAT Tyr	GAA Glu	CCA Pro	GTT Val	AAC Asn 125	AGC Ser	AGA Arg	TTG Leu	923
TCA Ser	GAT Asp 130	ATA Ile	TTC Phe	CGG Arg	GTG Val	GTC Val 135	CCA Pro	TTC Phe	ATA Ile	TCA Ser	GAT Asp 140	GTT Val	TTT Phe	CAG Gln	CAA Gln	971
GTG Val 145	GAG Glu	CAC His	ATT Ile	CCC Pro	AAA Lys 150	GGG Gly	AAC Asn	AAC Asn	TGC Cys	CTG Leu 155	GAT Asp	GCA Ala	GCG Ala	AAG Lys	GCC Ala 160	1019
TGC Cys	AAC Asn	CTC Leu	GAC Asp	GAC Asp 165	ATT Ile	TGC Cys	AAG Lys	AAG Lys	TAC Tyr 170	AGG Arg	TCG Ser	GCG Ala	TAC Tyr	ATC Ile 175	ACC Thr	1067
CCG Pro	TGC Cys	ACC Thr	ACC Thr 180	AGC Ser	GTG Val	TCC Ser	AAC Asn	GAT Asp 185	GTC Val	TGC Cys	AAC Asn	CGC Arg	CGC Arg 190	AAG Lys	TGC Cys	1115
CAC His	AAG Lys	GCC Ala 195	CTC Leu	CGG Arg	CAG Gln	TTC Phe	TTT Phe 200	GAC Asp	AAG Lys	GTC Val	CCG Pro	GCC Ala 205	AAG Lys	CAC His	AGC Ser	1163
TAC Tyr	GGA Gly 210	ATG Met	CTC Leu	TTC Phe	TGC Cys	TCC Ser 215	TGC Cys	CGG Arg	GAC Asp	ATC Ile	GCC Ala 220	TGC Cys	ACA Thr	GAG Glu	CGG Arg	1211
AGG Arg 225	CGA Arg	CAG Gln	ACC Thr	ATC Ile	GTG Val 230	CCT Pro	GTG Val	TGC Cys	TCC Ser	TAT Tyr 235	GAA Glu	GAG Glu	AGG Arg	GAG Glu	AAG Lys 240	1259
CCC Pro	AAC Asn	TGT Cys	TTG Leu	AAT Asn 245	TTG Leu	CAG Gln	GAC Asp	TCC Ser	TGC Cys 250	AAG Lys	ACG Thr	AAT Asn	TAC Tyr	ATC Ile 255	TGC Cys	1307
AGA Arg	TCT Ser	CGC Arg	CTT Leu 260	GCG Ala	GAT Asp	TTT Phe	TTT Phe	ACC Thr 265	AAC Asn	TGC Cys	CAG Gln	CCA Pro	GAG Glu 270	TCA Ser	AGG Arg	1355
TCT	GTC	AGC	AGC	TGT	CTA	AAG	GAA	AAC	TAC	GCT	GAC	TGC	CTC	СТС	GCC	1403

Ser	Val	Ser 275	Ser	Cys	Leu	Lys	Glu 280	Asn	Tyr	Ala	Asp	Cys 285	Leu	Leu	Ala	
TAC Tyr	TCG Ser 290	GGG Gly	CTT Leu	ATT Ile	GGC Gly	ACA Thr 295	GTC Val	ATG Met	ACC Thr	CCC Pro	AAC Asn 300	TAC Tyr	ATA Ile	GAC Asp	TCC Ser	1451
AGT Ser 305	AGC Ser	CTC Leu	AGT Ser	GTG Val	GCC Ala 310	CCA Pro	TGG Trp	TGT Cys	GAC Asp	TGC Cys 315	AGC Ser	AAC Asn	AGT Ser	GGG Gly	AAC Asn 320	1499
GAC Asp	CTA Leu	GAA Glu	GAG Glu	TGC Cys 325	TTG Leu	AAA Lys	TTT Phe	TTG Leu	AAT Asn 330	TTC Phe	TTC Phe	AAG Lys	GAC Asp	AAT Asn 335	ACA Thr	1547
TGT Cys	CTT Leu	AAA Lys	AAT Asn 340	GCA Ala	ATT Ile	CAA Gln	GCC Ala	TTT Phe 345	GGC Gly	AAT Asn	GGC Gly	TCC Ser	GAT Asp 350	GTG Val	ACC Thr	1595
GTG Val	TGG Trp	CAG Gln 355	CCA Pro	GCC Ala	TTC Phe	CCA Pro	GTA Val 360	CAG Gln	ACC Thr	ACC Thr	ACT Thr	GCC Ala 365	ACT Thr	ACC Thr	ACC Thr	1643
ACT Thr	GCC Ala 370	CTC Leu	CGG Arg	GTT Val	AAG Lys	AAC Asn 375	AAG Lys	CCC Pro	CTG Leu	GGG Gly	CCA Pro 380	GCA Ala	GGG Gly	TCT Ser	GAG Glu	1691
AAT Asn 385	GAA Glu	ATT Ile	CCC Pro	ACT Thr	CAT His 390	GTT Val	TTG Leu	CCA Pro	CCG Pro	TGT Cys 395	GCA Ala	AAT Asn	TTA Leu	CAG Gln	GCA Ala 400	1739
CAG Gln	AAG Lys	CTG Leu	AAA Lys	TCC Ser 405	AAT Asn	GTG Val	TCG Ser	GGC Gly	AAT Asn 410	ACA Thr	CAC His	CTC Leu	TGT Cys	ATT Ile 415	TCC Ser	1787
AAT Asn	GGT Gly	AAT Asn	TAT Tyr 420	GAA Glu	AAA Lys	GAA Glu	GGT Gly	CTC Leu 425	GGT Gly	GCT Ala	TCC Ser	AGC Ser	CAC His 430	ATA Ile	ACC Thr	1835
ACA Thr	AAA Lys	TCA Ser 435	ATG Met	GCT Ala	GCT Ala	CCT Pro	CCA Pro 440	AGC Ser	TGT Cys	GGT Gly	CTG Leu	AGC Ser 445	CCA Pro	CTG Leu	CTG Leu	1883
GTC Val	CTG Leu 450	GTG Val	GTA Val	ACC Thr	GCT Ala	CTG Leu 455	TCC Ser	ACC Thr	CTA Leu	TTA Leu	TCT Ser 460	TTA Leu	ACA Thr	GAA Glu		1928
A																1929

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu LA TLYFALPLLNLL M V

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser 50 60 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
70 75 80 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu 85 90 95 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly. 105 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala 150 Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys 185 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg 215 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg 265 Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala 280 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser 295 Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn 310 Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr 330 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Ala Thr Thr Thr

3	55	360	365
Thr Ala L 370		sn Lys Pro Leu Gly Pro 75 380	Ala Gly Ser Glu
Asn Glu I 385	le Pro Thr His V 390	al Leu Pro Pro Cys Ala 395	Asn Leu Gln Ala 400
Gln Lys L	eu Lys Ser Asn V 405	al Ser Gly Asn Thr His 410	Leu Cys Ile Ser 415
Asn Gly A	asn Tyr Glu Lys G 420	lu Gly Leu Gly Ala Ser 425	Ser His Ile Thr 430
	Ser Met Ala Ala P 35	ro Pro Ser Cys Gly Leu 440	Ser Pro Leu Leu 445
Val Leu V 450		eu Ser Thr Leu Leu Ser 55 460	Leu Thr Glu
(2) INFOR	RMATION FOR SEQ I	D NO:13:	
(ii) (ix) Figure (ix)	5 Hsgr-29a" FEATURE: (A) NAME/KEY: C (B) LOCATION: 2	base pairs ic acid S: single inear DNA sisc_feature699 MATION: /note= "1 to 69	99 is 814 to 1512 of
G TCG GCG	TAC ATC ACC CCG	TGC ACC ACC AGC GTG TG Cys Thr Thr Ser Val Se	er Asn Asp Val
1	5	10	15
TGC AAC C Cys Asn A	CGC CGC AAG TGC C Arg Arg Lys Cys H 20	AC AAG GCC CTC CGG CAG is Lys Ala Leu Arg Gln 25	TTC TTT GAC AAG 94 Phe Phe Asp Lys 30
GTC CCG G Val Pro A	GCC AAG CAC AGC T Ala Lys His Ser T 35	PAC GGA ATG CTC TTC TGC Pyr Gly Met Leu Phe Cys 40	TCC TGC CGG GAC 142 Ser Cys Arg Asp 45
ATC GCC T	rgc ACA GAG CGG A Cys Thr Glu Arg A 50	AGG CGA CAG ACC ATC GTG Arg Arg Gln Thr Ile Val 55	CCT GTG TGC TCC 190 Pro Val Cys Ser 60
TAT GAA G Tyr Glu G 65	GAG AGG GAG AAG C Glu Arg Glu Lys P	CC AAC TGT TTG AAT TTG Pro Asn Cys Leu Asn Leu 70 75	CAG GAC TCC TGC 238 Gln Asp Ser Cys

AAG Lys 80	ACG Thr	AAT Asn	TAC Tyr	ATC Ile	TGC Cys 85	AGA Arg	TCT Ser	CGC Arg	CTT Leu	GCG Ala 90	GAT Asp	TTT Phe	TTT Phe	ACC Thr	AAC Asn 95	286
TGC Cys	CAG Gln	CCA Pro	GAG Glu	TCA Ser 100	AGG Arg	TCT Ser	GTC Val	AGC Ser	AGC Ser 105	TGT Cys	CTA Leu	AAG Lys	GAA Glu	AAC Asn 110	TAC Tyr	334
GCT Ala	GAC Asp	TGC Cys	CTC Leu 115	CTC Leu	GCC Ala	TAC Tyr	TCG Ser	GGG Gly 120	CTT Leu	ATT Ile	GGC Gly	ACA Thr	GTC Val 125	ATG Met	ACC Thr	382
CCC Pro	AAC Asn	TAC Tyr 130	ATA Ile	GAC Asp	TCC Ser	AGT Ser	AGC Ser 135	CTC Leu	AGT Ser	GTG Val	GCC Ala	CCA Pro 140	TGG Trp	TGT Cys	GAC Asp	430
TGC Cys	AGC Ser 145	AAC Asn	AGT Ser	GGG Gly	AAC Asn	GAC Asp 150	CTA Leu	GAA Glu	GAG Glu	TGC Cys	TTG Leu 155	AAA Lys	TTT Phe	TTG Leu	AAT Asn	478
TTC Phe 160	TTC Phe	AAG Lys	GAC Asp	AAT Asn	ACA Thr 165	TGT Cys	CTT Leu	AAA Lys	AAT Asn	GCA Ala 170	ATT Ile	CAA Gln	GCC Ala	TTT Phe	GGC Gly 175	526
AAT Asn	GGC Gly	TCC Ser	GAT Asp	GTG Val 180	ACC Thr	GTG Val	TGG Trp	CAG Gln	CCA Pro 185	GCC Ala	TTC Phe	CCA Pro	GTA Val	CAG Gln 190	ACC Thr	574
ACC Thr	ACT Thr	GCC Ala	GCT Ala 195	ACC Thr	ACC Thr	ACT Thr	GCC Ala	CTC Leu 200	CGG Arg	GTT Val	AAG Lys	AAC Asn	AAG Lys 205	CCC Pro	CTG Leu	622
GGG Gly	CCA Pro	GCA Ala 210	GGG Gly	TCT Ser	GAG Glu	AAT Asn	GAA Glu 215	ATT Ile	CCC Pro	ACT Thr	CAT His	GTT Val 220	TTG Leu	CCA Pro	CCG Pro	670
	GCA Ala 225								AA							699

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 amino acids
 - (B) TYPE: amino acid (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys 1 5 10 15

Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val 20 25 30

Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile $35 \hspace{1cm} 40 \hspace{1cm} 45$

Ala Cys Thr Glu Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr 50 55 60

Glu 65	Glu	Arg	Glu	Lys	Pro 70	Asn	Cys	Leu	Asn	Leu 75	Gln	Asp	Ser	Cys	Lys 80
Thr	Asn	Tyr	Ile	Cys 85	Arg	Ser	Arg	Leu	Ala 90	Asp	Phe	Phe	Thr	Asn 95	Cys
Gln	Pro	Glu	Ser 100	Arg	Ser	Val	Ser	Ser 105	Cys	Leu	Lys	Glu	Asn 110	Tyr	Ala
Asp	Cys	Leu 115	Leu	Ala	Tyr	Ser	Gly 120	Leu	Ile	Gly	Thr	Val 125	Met	Thr	Pro
Asn	Tyr 130	Ile	Asp	Ser	Ser	Ser 135	Leu	Ser	Val	Ala	Pro 140	Trp	Cys	Asp	Cys
Ser 145	Asn	Ser	Gly	Asn	Asp 150	Leu	Glu	Glu	Cys	Leu 155	Lys	Phe	Leu	Asn	Phe 160
Phe	Lys	Asp	Asn	Thr 165	Cys	Leu	Lys	Asn	Ala 170	Ile	Gln	Ala	Phe	Gly 175	Asn
Gly	Ser	Asp	Val 180	Thr	Val	Trp	Gln	Pro 185	Ala	Phe	Pro	Val	Gln 190	Thr	Thr
Thr	Ala	Ala 195	Thr	Thr	Thr	Ala	Leu 200	Arg	Val	Lys	Asn	Lys 205	Pro	Leu	Gly
Pro	Ala 210	Gly	Ser	Glu	Asn	Glu 215	Ile	Pro	Thr	His	Val 220	Leu	Pro	Pro	Cys
Ala	Asn	Leu	Gln	Ala	Gln	Lys	Leu								

- (2) INFORMATION FOR SEQ ID NO:15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2157 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:

 - (A) NAME/KEY: CDS
 (B) LOCATION: 2..886
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..2157
 - (D) OTHER INFORMATION: /note= "1 to 2157 is 814 to 2971 of Figure 5 29brc"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
- 46 G TCG GCG TAC ATC ACC CCG TGC ACC ACC AGC GTG TCC AAT GAT GTC Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val 1
- TGC AAC CGC CGC AAG TGC CAC AAG GCC CTC CGG CAG TTC TTT GAC AAG 94 Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys 20

GTC Val	CCG Pro	GCC Ala	AAG Lys 35	CAC His	AGC Ser	TAC Tyr	GGA Gly	ATG Met 40	CTC Leu	TTC Phe	TGC Cys	TCC Ser	TGC Cys 45	CGG Arg	GAC Asp	142
ATC Ile	GCC Ala	TGC Cys 50	ACA Thr	GAG Glu	CGG Arg	AGG Arg	CGA Arg 55	CAG Gln	ACC Thr	ATC Ile	GTG Val	CCT Pro 60	GTG Val	TGC Cys	TCC Ser	190
TAT Tyr	GAA Glu 65	GAG Glu	AGG Arg	GAG Glu	AAG Lys	CCC Pro 70	AAC Asn	TGT Cys	TTG Leu	AAT Asn	TTG Leu 75	CAG Gln	GAC Asp	TCC Ser	TGC Cys	238
AAG Lys 80	ACG Thr	AAT Asn	TAC Tyr	ATC Ile	TGC Cys 85	AGA Arg	TCT Ser	CGC Arg	CTT Leu	GCG Ala 90	GAT Asp	TTT Phe	TTT Phe	ACC Thr	AAC Asn 95	286
TGC Cys	CAG Gln	CCA Pro	GAG Glu	TCA Ser 100	AGG Arg	TCT Ser	GTC Val	AGC Ser	AGC Ser 105	TGT Cys	CTA Leu	AAG Lys	GAA Glu	AAC Asn 110	TAC Tyr	334
GCT Ala	GAC Asp	TGC Cys	CTC Leu 115	CTC Leu	GCC Ala	TAC Tyr	TCG Ser	GGG Gly 120	CTT Leu	ATT Ile	GGC Gly	ACA Thr	GTC Val 125	ATG Met	ACC Thr	382
CCC Pro	AAC Asn	TAC Tyr 130	ATA Ile	GAC Asp	TCC Ser	AGT Ser	AGC Ser 135	CTC Leu	AGT Ser	GTG Val	GCC Ala	CCA Pro 140	TGG Trp	TGT Cys	GAC Asp	430
TGC Cys	AGC Ser 145	AAC Asn	AGT Ser	GGG Gly	AAC Asn	GAC Asp 150	CTA Leu	GAA Glu	GAG Glu	TGC Cys	TTG Leu 155	AAA Lys	TTT Phe	TTG Leu	AAT Asn	478
TTC Phe 160	TTC Phe	AAG Lys	GAC Asp	AAT Asn	ACA Thr 165	TGT Cys	CTT Leu	AAA Lys	AAT Asn	GCA Ala 170	ATT Ile	CAA Gln	GCC Ala	TTT Phe	GGC Gly 175	526
AAT Asn	GGC Gly	TCC Ser	GAT Asp	GTG Val 180	ACC Thr	GTG Val	TGG Trp	CAG Gln	CCA Pro 185	GCC Ala	TTC Phe	CCA Pro	GTA Val	CAG Gln 190	ACC Thr	574
ACC Thr	ACT Thr	GCC Ala	GCT Ala 195	ACC Thr	ACC Thr	ACT Thr	GCC Ala	CTC Leu 200	CGG Arg	GTT Val	AAG Lys	AAC Asn	AAG Lys 205	CCC Pro	CTG Leu	622
GGG Gly	CCA Pro	GCA Ala 210	GGG Gly	TCT Ser	GAG Glu	AAT Asn	GAA Glu 215	ATT Ile	CCC Pro	ACT Thr	CAT His	GTT Val 220	TTG Leu	CCA Pro	CCG Pro	670
TGT Cys	GCA Ala 225	AAT Asn	TTA Leu	CAG Gln	GCA Ala	CAG Gln 230	AAG Lys	CTG Leu	AAA Lys	TCC Ser	AAT Asn 235	GTG Val	TCG Ser	GGC Gly	AAT Asn	718
ACA Thr 240	CAC His	CTC Leu	TGT Cys	ATT Ile	TCC Ser 245	AAT Asn	GGT Gly	AAT Asn	TAT Tyr	GAA Glu 250	AAA Lys	GAA Glu	GGT Gly	CTC Leu	GGT Gly 255	766
GCT Ala	TCC Ser	AGC Ser	CAC His	ATA Ile 260	ACC Thr	ACA Thr	AAA Lys	TCA Ser	ATG Met 265	GCT Ala	GCT Ala	CCT Pro	CCA Pro	AGC Ser 270	TGT Cys	814
GGT Gly	CTG Leu	AGC Ser	CCA Pro 275	CTG Leu	CTG Leu	GTC Val	CTG Leu	GTG Val 280	GTA Val	ACC Thr	GCT Ala	CTG Leu	TCC Ser 285	ACC Thr	CTA Leu	862

	A ACA GAA AO 1 Thr Glu Th)		CTGCATTAAA A	AAAATACAAT A	ATGGACATGT	916
AAAAAGACAA	AAACCAAGTT	ATCTGTTTCC	TGTTCTCTTG	TATAGCTGAA	ATTCCAGTTT	976
AGGAGCTCAG	TTGAGAAACA	GTTCCATTCA	ACTGGAACAT	TTTTTTTTTT	CCTTTTAAGA	1036
AAGCTTCTTG	TGATCCTTCG	GGGCTTCTGT	GAAAAACCTG	ATGCAGTGCT	CCATCCAAAC	1096
TCAGAAGGCT	TTGGGATATG	CTGTATTTTA	AAGGGACAGT	TTGTAACTTG	GGCTGTAAAG	1156
CAAACTGGGG	CTGTGTTTTC	GATGATGATG	ATCATCATGA	TCATGATNNN	NNNNNNNNN	1216
NNNNNNNNN	NNNNNNNNN	NNNNNGATT	TTAACAGTTT	TACTTCTGGC	CTTTCCTAGC	1276
TAGAGAAGGA	GTTAATATTT	CTAAGGTAAC	TCCCATATCT	CCTTTAATGA	CATTGATTTC	1336
TAATGATATA	AATTTCAGCC	TACATTGATG	CCAAGCTTTT	TTGCCACAAA	GAAGATTCTT	1396
ACCAAGAGTG	GGCTTTGTGG	AAACAGCTGG	TACTGATGTT	CACCTTTATA	TATGTACTAG	1456
CATTTTCCAC	GCTGATGTTT	ATGTACTGTA	AACAGTTCTG	CACTCTTGTA	CAAAAGAAAA	1516
AACACCTGTC	ACATCCAAAT	ATAGTATCTG	TCTTTTCGTC	AAAATAGAGA	GTGGGGAATG	1576
AGTGTGCCGA	TTCAATACCT	CAATCCCTGA	ACGACACTCT	CCTAATCCTA	AGCCTTACCT	1636
GAGTGAGAAG	CCCTTTACCT	AACAAAAGTC	CAATATAGCT	GAAATGTCGC	TCTAATACTC	1696
TTTACACATA	TGAGGTTATA	TGTAGAAAAA	AATTTTACTA	CTAAATGATT	TCAACTATTG	1756
GCTTTCTATA	TTTTGAAAGT	AATGATATTG	TCTCATTTTT	TTACTGATGG	TTTAATACAA	1816
AATACACAGA	GCTTGTTTCC	CCTCATAAGT	AGTGTTCGCT	CTGATATGAA	CTTCACAAAT	1876
ACAGCTCATC	AAAAGCAGAC	TCTGAGAAGC	CTCGTGCTGT	AGCAGAAAGT	TCTGCATCAT	1936
GTGACTGTGG	ACAGGCAGGA	GGAAACAGAA	CAGACAAGCA	TTGTCTTTTG	TCATTGCTCG	1996
AAGTGCAAGC	GTGCATACCT	GTGGAGGGAA	CTGGTGGCTG	CTTGTAAATG	TTCTGCAGCA	2056
TCTCTTGACA	CACTTGTCAT	GACACAATCC	AGTACCTTGG	TTTTCAGGTT	ATCTGACAAA	2116
GGCAGCTTTG	ATTGGGACAT	GGAGGCATGG	GCAGGCCGGA	A		2157

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys 1 5 10 15

Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val 20 25 30

Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys 90 Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys 135 Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr 185 Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly 205 Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala 250 Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly 265 Leu Ser Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu 280 Ser Leu Thr Glu Thr Ser 295 290

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 659 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 2..658

- (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..659
 (D) OTHER INFORMATION: /note= "1 to 659 is 1033 to 1691 of Figure 5 Hsgr-21ar"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

G AAT TTG CAG GAC Asn Leu Gln Asp 1	TCC TGC AAG AG Ser Cys Lys Tl 5	CG AAT TAC ATC hr Asn Tyr Ile 10	TGC AGA TCT CGC Cys Arg Ser Arg 15	•
CTT GCG GAT TTT TT Leu Ala Asp Phe Ph	T ACC AAC TGC e Thr Asn Cys 0	CAG CCA GAG TC Gln Pro Glu Se 25	CA AGG TCT GTC A er Arg Ser Val S 30	GC 94 er
AGC TGT CTA AAG GA Ser Cys Leu Lys Gl 35	A AAC TAC GCT u Asn Tyr Ala	GAC TGC CTC CT Asp Cys Leu Le 40	CC GCC TAC TCG G eu Ala Tyr Ser G 45	GGG 142 Hy
CTT ATT GGC ACA GT Leu Ile Gly Thr Va 50	C ATG ACC CCC 1 Met Thr Pro 55	AAC TAC ATA GA Asn Tyr Ile As	AC TCC AGT AGC C Sp Ser Ser Ser I 60	TC 190 eu
AGT GTG GCC CCA TG Ser Val Ala Pro Tr 65	G TGT GAC TGC p Cys Asp Cys 70	Ser Asn Ser Gl	GG AAC GAC CTA G .y Asn Asp Leu G '5	AA 238 Ju
GAG TGC TTG AAA TT Glu Cys Leu Lys Ph 80	T TTG AAT TTC e Leu Asn Phe 85	TTC AAG GAC AA Phe Lys Asp As 90	AT ACA TGT CTT A on Thr Cys Leu I	AA 286 ys 95
AAT GCA ATT CAA GC Asn Ala Ile Gln Al 10	a Phe Gly Asn	GGC TCC GAT GT Gly Ser Asp Va 105	TG ACC GTG TGG C il Thr Val Trp G 110	AG 334 Sln
CCA GCC TTC CCA GT Pro Ala Phe Pro Va 115	A CAG ACC ACC 1 Gln Thr Thr	ACT GCC ACT AC Thr Ala Thr Th 120	CC ACC ACT GCC C ar Thr Thr Ala I 125	TC 382 eu
CGG GTT AAG AAC AA Arg Val Lys Asn Ly 130	G CCC CTG GGG s Pro Leu Gly 135	CCA GCA GGG TC Pro Ala Gly Se	CT GAG AAT GAA A er Glu Asn Glu I 140	TT 430
CCC ACT CAT GTT TT Pro Thr His Val Le 145	G CCA CCG TGT u Pro Pro Cys 150	GCA AAT TTA CA Ala Asn Leu Gl 15	n Ala Gln Lys I	ETG 478 Jeu
AAA TCC AAT GTG TC Lys Ser Asn Val Se 160	G GGC AAT ACA r Gly Asn Thr 165	CAC CTC TGT AT His Leu Cys II 170	e Ser Asn Gly A	AT 526 ASD .75
TAT GAA AAA GAA GC Tyr Glu Lys Glu Gl 18	y Leu Gly Ala	TCC AGC CAC AT Ser Ser His II 185	TA ACC ACA AAA T Le Thr Thr Lys S 190	CCA 574 Ser
ATG GCT GCT CCT CC Met Ala Ala Pro Pr 195	A AGC TGT GGT O Ser Cys Gly	CTG AGC CCA CT Leu Ser Pro Le 200	CG CTG GTC CTG G Eu Leu Val Leu V 205	GTG 622 Val

659

GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA A Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu 210 215

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu
1 10 15

Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser 20 25 30

Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu
35 40

Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser 50 60

Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu 65 70 75 80

Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn 85 90 95

Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro 100 105 110

Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Ala Leu Arg 115 120 125

Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro 130 135 140

Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys 145 150 155 160

Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr 165 170 175

Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met 180 185 190

Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val 195 200 205

Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu 210 215

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 (B) LOCATION: 3..629
- (ix) FEATURE:
- (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..630
 (D) OTHER INFORMATION: /note= "1 to 630 is 1062 to 1691 of Figure 5 Hsgr-21br"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AC I	ATC 1 Ile (TGC A	AGA '	TCT (Ser /	CGC (Arg 1 5	CTT (Leu A	GCG (GAT ' Asp :	TTT '	TTT I Phe ' 10	ACC I	AAC (Asn (rgc (Cys (CAG (Gln 1	CCA Pro 15	47
GAG Glu	TCA Ser	AGG Arg	TCT Ser	GTC Val 20	AGC Ser	AGC Ser	TGT Cys	CTA Leu	AAG Lys 25	GAA Glu	AAC Asn	TAC Tyr	GCT Ala	GAC Asp 30	TGC Cys	95
CTC Leu	CTC Leu	GCC Ala	TAC Tyr 35	TCG Ser	GGG Gly	CTT Leu	ATT Ile	GGC Gly 40	ACA Thr	GTC Val	ATG Met	ACC Thr	CCC Pro 45	AAC Asn	TAC Tyr	143
ATA Ile	GAC Asp	TCC Ser 50	AGT Ser	AGC Ser	CTC Leu	AGT Ser	GTG Val 55	GCC Ala	CCA Pro	TGG Trp	TGT Cys	GAC Asp 60	TGC Cys	AGC Ser	AAC Asn	191
AGT Ser	GGG Gly 65	AAC Asn	GAC Asp	CTA Leu	GAA Glu	GAG Glu 70	TGC Cys	TTG Leu	AAA Lys	TTT Phe	TTG Leu 75	AAT Asn	TTC Phe	TTC Phe	AAG Lys	239
GAC Asp 80	AAT Asn	ACA Thr	TGT Cys	CTT Leu	AAA Lys 85	AAT Asn	GCA Ala	ATT Ile	CAA Gln	GCC Ala 90	TTT Phe	GGC Gly	AAT Asn	GGC Gly	TCC Ser 95	287
GAT Asp	GTG Val	ACC Thr	GTG Val	TGG Trp 100	CAG Gln	CCA Pro	GCC Ala	TTC Phe	CCA Pro 105	GTA Val	CAG Gln	ACC Thr	ACC Thr	ACT Thr 110	GCC Ala	335
ACT Thr	ACC Thr	ACC Thr	ACT Thr 115	GCC Ala	CTC Leu	CGG Arg	GTT Val	AAG Lys 120	AAC Asn	AAG Lys	CCC Pro	CTG Leu	GGG Gly 125	CCA Pro	GCA Ala	383
GGG Gly	TCT Ser	GAG Glu 130	AAT Asn	GAA Glu	ATT Ile	CCC Pro	ACT Thr 135	CAT His	GTT Val	TTG Leu	CCA Pro	CCG Pro 140	TGT Cys	GCA Ala	AAT Asn	431
TTA Leu	CAG Gln 145	GCA Ala	CAG Gln	AAG Lys	CTG Leu	AAA Lys 150	TCC Ser	AAT Asn	GTG Val	TCG Ser	GGC Gly 155	AAT Asn	ACA Thr	CAC His	CTC Leu	479
TGT Cys 160	ATT Ile	TCC Ser	AAT Asn	GGT Gly	AAT Asn 165	TAT Tyr	GAA Glu	AAA Lys	GAA Glu	GGT Gly 170	CTC Leu	GGT Gly	GCT Ala	TCC Ser	AGC Ser 175	527
CAC His	ATA Ile	ACC Thr	ACA Thr	AAA Lys	TCA Ser	ATG Met	GCT Ala	GCT Ala	CCT Pro	CCA Pro	AGC Ser	TGT Cys	GGT Gly	CTG Leu	AGC Ser	575

CCA CTG CTG GTC CTG GTG GTA ACC GCT CTG TCC ACC CTA TTA TCT TTA Pro Leu Leu Val Leu Val Thr Ala Leu Ser Thr Leu Leu Ser Leu 205

ACA GAA A Thr Glu

- (2) INFORMATION FOR SEQ ID NO:20:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 209 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu
1 5 10 15

Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu 20 25 30

Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile 35 40 45

Asp Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser 50 55 60

Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp 65 70 75 80

Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp 85 90 95

Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr 100 105 110

Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly 115 120 125

Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu 130 135 140

Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys 145 150 155 160

Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His 165 170 175

Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro 180 185 190

Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr 195 200 205

Glu

(2) INFORMATION FOR SEQ ID NO:21: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1075 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 (B) LOCATION: 2..445
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature (B) LOCATION: 1..1075
- (D) OTHER INFORMATION: /note= "1 to 1075 is 1255 to 2330 of Figure 5 Hsgr-2"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

T GGG AAC GAC C Gly Asn Asp I 1	TA GAA GAG TGC eu Glu Glu Cys 5	TTG AAA TTT TT Leu Lys Phe Le 10	rG AAT TTC TTC AA eu Asn Phe Phe Ly	AG 46 /s L5
GAC AAT ACA TGT Asp Asn Thr Cys	CTT AAA AAT G Leu Lys Asn A 20	CA ATT CAA GCC la Ile Gln Ala 25	TTT GGC AAT GGC Phe Gly Asn Gly 30	TCC 94 Ser
GAT GTG ACC GTG Asp Val Thr Val	Trp Gln Pro A	CC TTC CCA GTA la Phe Pro Val 40	CAG ACC ACC ACT Gln Thr Thr 45	GCC 142 Ala
ACT ACC ACC ACT Thr Thr Thr 50	Ala Leu Arg V	TT AAG AAC AAG al Lys Asn Lys 55	CCC CTG GGG CCA Pro Leu Gly Pro 60	GCA 190 Ala
GGG TCT GAG AAT Gly Ser Glu Asr 65	GAA ATT CCC AG Glu Ile Pro Ti 70	CT CAT GTT TTG nr His Val Leu	CCA CCG TGT GCA Pro Pro Cys Ala 75	AAT 238 Asn
TTA CAG GCA CAG Leu Gln Ala Glr 80	AAG CTG AAA T Lys Leu Lys S 85	CC AAT GTG TCG er Asn Val Ser 90	GGC AAT ACA CAC Gly Asn Thr His	CTC 286 Leu 95
TGT ATT TCC AAT	GGT AAT TAT G Gly Asn Tyr G 100	AA AAA GAA GGT lu Lys Glu Gly 105	CTC GGT GCT TCC Leu Gly Ala Ser 110	AGC 334 Ser
CAC ATA ACC ACA His Ile Thr Thr 115	Lys Ser Met A	CT GCT CCT CCA la Ala Pro Pro 120	AGC TGT GGT CTG Ser Cys Gly Leu 125	AGC 382 Ser
CCA CTG CTG GTC Pro Leu Leu Val 130	. Leu Val Val T	CC GCT CTG TCC hr Ala Leu Ser 35	ACC CTA TTA TCT Thr Leu Leu Ser 140	TTA 430 Leu
ACA GAA ACA TCA Thr Glu Thr Sen 145		A AAAATACAAT A	TGGACATGT AAAAAG	ACAA 485

AAACCAAGTT	ATCTGTTTCC	${\tt TGTTCTCTTG}$	TATAGCTGAA	ATTCCAGTTT	AGGAGCTCAG	545
TTGAGAAACA	GTTCCATTCA	ACTGGAACAT	$\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}\mathbf{T}$	CCTTTTAAGA	AAGCTTCTTG	605
TGATCCTTCG	GGGCTTCTGT	GAAAAACCTG	ATGCAGTGCT	CCATCCAAAC	TCAGAAGGCT	665
TTGGGATATG	CTGTATTTTA	AAGGGACAGT	TTGTAACTTG	GGCTGTAAAG	CAAACTGGGG	725
СТСТСТТТТС	GATGATGATG	ATCATCATGA	TCATGATNNN	NNNNNNNNN	NNNNNNNNN	785
NNNNNNNNN	NNNNNGATT	TTAACAGTTT	TACTTCTGGC	CTTTCCTAGC	TAGAGAAGGA	845
GTTAATATTT	CTAAGGTAAC	TCCCATATCT	CCTTTAATGA	CATTGATTTC	TAATGATATA	905
AATTTCAGCC	TACATTGATG	CCAAGCTTTT	TTGCCACAAA	GAAGATTCTT	ACCAAGAGTG	965
GGCTTTGTGG	AAACAGCTGG	TACTGATGTT	CACCTTTATA	TATGTACTAG	CATTTTCCAC	1025
GCTGATGTTT	ATGTACTGTA	AACAGTTCTG	CACTCTTGTA	CAAAAGAAAA		1075

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp

Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp

Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr

Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly

Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu

Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys

Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His 105

Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro 115

Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr 140

Glu Thr Ser * 145

(2) INFORMATION FOR SEQ ID NO:23:

(:	(I (C	QUENC A) LE B) TY C) ST O) TO	ENGTH (PE: RANI	H: 10 nucl	059 l leic ESS:	oase ació sino	pai: 1	rs							
(i:	i) MOI	LECUI	LE TY	PE:	CDN	A									
(i:		ATURE A) NA B) LO	ME/F			428									
	(1	A) NA B) LO C) OI	AME/F CATI THER	ON:	11	1059			"1 1	to 10)59 ±	is 1	272 1	to 233	0
	i) SE(
AG TGC Cys 1	TTG A	AAA 1 Lys E	rrr 1 Phe I	rTG A Leu A 5	AAT 1 Asn 1	TTC T	Phe	AAG (Lys 1	GAC A Asp A	AAT A Asn :	ACA T	rgt Cys	CTT I	AAA Lys 15	47
AAT GCA	A ATT a Ile	CAA Gln	GCC Ala 20	TTT Phe	GGC Gly	AAT Asn	GGC Gly	TCC Ser 25	GAT Asp	GTG Val	ACC Thr	GTG Val	TGG Trp 30	CAG Gln	95
CCA GCO	C TTC a Phe	CCA Pro 35	GTA Val	CAG Gln	ACC Thr	ACC Thr	ACT Thr 40	GCC Ala	ACT Thr	ACC Thr	ACC Thr	ACT Thr 45	Ala	CTC Leu	143
CGG GT' Arg Va	r AAG l Lys 50	AAC Asn	AAG Lys	CCC Pro	CTG Leu	GGG Gly 55	CCA Pro	GCA Ala	GGG Gly	TCT Ser	GAG Glu 60	AAT Asn	GAA Glu	ATT Ile	191
CCC ACT	r His	GTT Val	TTG Leu	CCA Pro	CCG Pro 70	TGT Cys	GCA Ala	AAT Asn	TTA Leu	CAG Gln 75	GCA Ala	CAG Gln	AAG Lys	CTG Leu	239
AAA TCC Lys Se: 80	C AAT r Asn	GTG Val	TCG Ser	GGC Gly 85	AAT Asn	ACA Thr	CAC His	CTC Leu	TGT Cys 90	ATT Ile	TCC Ser	AAT Asn	GGT Gly	AAT Asn 95	287
TAT GAZ Tyr Gl	A AAA 1 Lys	GAA Glu	GGT Gly 100	CTC Leu	GGT Gly	GCT Ala	TCC Ser	AGC Ser 105	CAC His	ATA Ile	ACC Thr	ACA Thr	AAA Lys 110	TCA Ser	335
ATG GC	r GCT a Ala	CCT Pro 115	CCA Pro	AGC Ser	TGT Cys	GGT Gly	CTG Leu 120	AGC Ser	CCA Pro	CTG Leu	CTG Leu	GTC Val 125	Leu	GTG Val	383
GTA ACC	C GCT r Ala 130	CTG Leu	TCC Ser	ACC Thr	CTA Leu	TTA Leu 135	TCT Ser	TTA Leu	ACA Thr	GAA Glu	ACA Thr 140	TCA Ser	TAG *		428
CTGCAT'	TAAA A	ΑΑΑΑ	TACAZ	AT AT	rgga	CATG	r aa	AAAG	ACAA	AAA	CCAA	3TT	ATCT	GTTTCC	488
TGTTCT	CTTG 7	ratac	GCTG/	AA A?	rtcc <i>i</i>	AGTT	r AG	GAGC'	rcag	TTG	AGAA	ACA	GTTC	CATTCA	548
ACTGGA	ልሮልጥ ባ	րդորդո	րդորդո	ኮጥ ጥረ	СТТ	гтаас	G AA	AGCT'	гстт	GTG	ATCC	rtt	GGGG	CTTCTG	608

TGAAAAACCT	GATGCAGTGC	TCCATCCAAA	CTCAGAAGGC	TTTGGGATAT	GCTGTATTTT	668
AAAGGGACAG	TTTGTAACTT	GGGCTGTAAA	GCAAACTGGG	GCTGTGTTTT	CGATGATGAT	728
GATGATCATG	ATGATGATCA	TCATGATCAT	GATGATGATC	ATCATGATCA	TGATGATGAT	788
TTTAACAGTT	TTACTTCTGG	CCTTTCCTAG	CTAGAGAAGG	AGTTAATATT	TCTAAGGTAA	848
СТСССАТАТС	TCCTTTAATG	ACATTGATTT	CTAATGATAT	AAATTTCAGC	CTACATTGAT	908
GCCAAGCTTT	TTTGCCACAA	AGAAGATTCT	TACCAAGAGT	GGGCTTTGTG	GAAACAGCTG	968
GTACTGATGT	TCACCTTTAT	ATATGTACTA	GCATTTTCCA	CGCTGATGTT	TATGTACTGT	1028
AAACAGTTCT	GCACTCTTGT	ACAAAAGAAA	A			1059

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn

Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro

Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Ala Leu Arg

Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro 50 55 60

Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys

Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr 85 90 95

Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met

Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val 120 115

Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser 130

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids(B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25: Gln Ser Cys Ser Thr Lys Tyr Arg Thr Leu
- (2) INFORMATION FOR SEQ ID NO:26:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26: Cys Lys Arg Gly Met Lys Lys Glu Lys Asn
- (2) INFORMATION FOR SEQ ID NO:27:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27: Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val
- (2) INFORMATION FOR SEQ ID NO:28:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids

 - (B) TYPE: amino acid(C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28: Cys Ser Tyr Glu Glu Arg Glu Arg Pro Asn
- (2) INFORMATION FOR SEQ ID NO:29:

	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: peptide	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:29:	
	Pro 1	Ala Pro Pro Val Gln Thr Thr Thr Ala Thr Thr Thr 5	
(2)	INFO	RMATION FOR SEQ ID NO:30:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
		SEQUENCE DESCRIPTION: SEQ ID NO:30:	21
		AT TTGCAGGACT C	21
(2)		RMATION FOR SEQ ID NO:31:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:31:	
СТС	CTCTC	TA AGCTTCTAAC CACAGCTTGG AGGAGC	36
(2)	INFO	RMATION FOR SEQ ID NO:32:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
CTCCTCTCTA AGCTTCTATG GGCTCAGACC ACAGCTT	37
(2) INFORMATION FOR SEQ ID NO:33:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
CTCCTCTCTA AGCTTCTACT TGTCATCGTC GTCCTTGTAG TCACCACAGC TTGGAGGAGC	60
(2) INFORMATION FOR SEQ ID NO:34:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34: CTCCTCTCTA AGCTTCTACT TGTCATCGTC GTCCTTGTAG TCTGGCTCAG ACCACAGCTT	60
44	
(2) INFORMATION FOR SEQ ID NO:35: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 4232 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 15872978	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:	
CATGAAGAA CCTCAGTAAG TCTCAGACTT GGCCCAAAGG AGCCCAACTA GTTACTCCCT	60
GGTCTGTTAC AGAGGATCTG GCTATTACAC TCAACAGCAA AAATTCAATT CAATCCCGCT	120
AAAGATATAA GAATCACTAG GAAKAATAAG CCAGAACTCA AGACAGAAAT AGCATTAAGT	180

AGTTCCTTCA GTACAGT	AG CAGAAGCTGG	CCACTCTACG	ACTCTAWAAG ACTCAGAAA	A 240
GCTTACTAGG GACCWCT	GG CATWCCGGTG	TCCTATGTGG	GGATTTCGTA ACGTCTTTC	300 a
GTCAGAAGCT GCCCTCA	AA TAGTTTCTTC	TCAAAACGGT	TTCAGGCTTT GTTAGAAAG	iG 360
GAAGACTTCA CTGCCAC	TT ACCCAGATCA	TCTACCCCAT	CCTTGGAATG AATGGGGAA	G 420
CTTCAGCCAC CCTACCA	GC ТССТААААТС	ACCAACTTGA	GAGAAAAACT ATAACGTTO	C 480
TCTACCAGTA CTTCAGG	GG TTAAAGAAAG	TCACAGAAGA	AAAGAACTCT GGGGAAAAC	A 540
GTCAAATTCG GCTATTA	GA CATTAGTTAC	AGGCCCCTGT	ACCTCTCCTC TAGAAACCC	T 600
GGGAGTACAC CCGCAGA	GA GAGAGAGCCC	AAGCCACCAA	GCAAAGTCAA CCAATCTGO	C 660
AAAGGGGCGT CCCACTG	GG CTTTCAGTCC	AAGAAGTGGA	TCCTGCTGGT TCGCAGTCT	rc 720
TCTTCTATCT CCTCACT	CC TATTTACCCT	TTGAAGTGGG	TACTGAATAG CCCGTTCCC	A 780
AGCAGAGGCC CTTTGTA	AC GGGGTGCTAC	AGTCGCCTGG	TGGAAACACC TTGGCAGAG	T 840
TGTTTGGTGC CAGGATG	GC CACTGAAGGC	ATCTGCTGTG	GACACACACA CACACACAC	A 900
CACACACACA CACACACAC	CA GAGAGAGGAG	AGAGAAAGAC	ACACGCACGC AGAGACACA	C 960
GGTCACTGGA ATTCCAT	'AG AAAAAAGTGA	GCCGAGCAAG	GGTTAGCGGG AGAAGATTT	T 1020
TTTGAATCTT GTCTTCG	CT TGGTGCGAAA	GAAGCGACTC	CAGTCTCTCG TCCTCGAAC	C 1080
TCCGACTGGA TTGTTCT	GG GCGCTGACAC	CCGTCTGTGG	ATTTCTTTTC TATTTGCAT	T 1140
TTATTCCGAC CCCCTCC	TC GCCGCTTCCT	TCCAGCCCTT	CACTCGCAAA TCGCCTCTC	T 1200
CCCCACCTCC CCAGGCC	CT CCTGGGAAGC	GCAGGGGAAT	TGGACCCGCG GGGACTCAC	G 1260
CCTTCCCGGA CGATTGG	GG GGAGGGCTGA	CCCCAGGACT	GGGCTGTTGG CTTAGAAAC	C 1320
CGATACACAG ATACGCG	AT ATTTGATTGT	AGCGGGCAAG	GGGGGCGTCG AGAGGCAGC	A 1380
GCCCATCGCC CGCCTCT	AC CCCACCCCT	CCAGCCAGAG	GCGAGAATCG CAGGACTCC	G 1440
GATCTTCATC GGGTGGA	TA GCTGGGATCT	CCGCATTGGA	TTTGGGGCTG ATTACCACT	G 1500
CTTGGCTATT ATTATTG	TG TTGTTACTAC	TATTATTTT	TTTTACCCAA GGGAGAAAC	SA 1560
CAAAAAAACG GTGGGAT	TTA TTTAAC ATG Met 1	. Ile Leu Ala	A AAC GTC TTC TGC CTC a Asn Val Phe Cys Lev 5	1613
TTC TTC TTT CTA GAPhe Phe Phe Phe Leu As	GAC ACC CTC Asp Thr Leu 15	CGC TCT TTG Arg Ser Leu 20	GCC AGC CCT TCC TCC Ala Ser Pro Ser Ser 25	1661
CTG CAG GGC CCC GA Leu Gln Gly Pro Gl 3	Leu His Gly	TGG CGC CCC Trp Arg Pro 35	CCA GTG GAC TGT GTC Pro Val Asp Cys Val 40	1709
CGG GCC AAT GAG CT Arg Ala Asn Glu Le 45	TGT GCC GCC Cys Ala Ala	GAA TCC AAC Glu Ser Asn 50	TGC AGC TCT CGC TAC Cys Ser Ser Arg Tyr 55	1757
CGC ACT CTG CGG CA Arg Thr Leu Arg Gl	TGC CTG GCA Cys Leu Ala	GGC CGC GAC Gly Arg Asp	CGC AAC ACC ATG CTG Arg Asn Thr Met Leu	1805

		60					65					70					
GCC Ala	AAC Asn 75	AAG Lys	GAG Glu	TGC Cys	CAG Gln	GCG Ala 80	GCC Ala	TTG Leu	GAG Glu	GTC Val	TTG Leu 85	CAG Gln	GAG Glu	AGC Ser	CCG Pro	18	53
CTG Leu 90	TAC Tyr	GAC Asp	TGC Cys	CGC Arg	TGC Cys 95	AAG Lys	CGG Arg	GGC Gly	ATG Met	AAG Lys 100	AAG Lys	GAG Glu	CTG Leu	CAG Gln	TGT Cys 105	19	01
CTG Leu	CAG Gln	ATC Ile	TAC Tyr	TGG Trp 110	AGC Ser	ATC Ile	CAC His	CTG Leu	GGG Gly 115	CTG Leu	ACC Thr	GAG Glu	GGT Gly	GAG Glu 120	GAG Glu	19	49
TTC Phe	TAC Tyr	GAA Glu	GCC Ala 125	TCC Ser	CCC Pro	TAT Tyr	GAG Glu	CCG Pro 130	GTG Val	ACC Thr	TCC Ser	CGC Arg	CTC Leu 135	TCG Ser	GAC Asp	19	97
ATC Ile	TTC Phe	AGG Arg 140	CTT Leu	GCT Ala	TCA Ser	ATC Ile	TTC Phe 145	TCA Ser	GGG Gly	ACA Thr	GGG Gly	GCA Ala 150	GAC Asp	CCG Pro	GTG Val	20	45
GTC Val	AGC Ser 155	GCC Ala	AAG Lys	AGC Ser	AAC Asn	CAT His 160	TGC Cys	CTG Leu	GAT Asp	GCT Ala	GCC Ala 165	AAG Lys	GCC Ala	TGC Cys	AAC Asn	20	93
CTG Leu 170	AAT Asn	GAC Asp	AAC Asn	TGC Cys	AAG Lys 175	AAG Lys	CTG Leu	CGC Arg	TCC Ser	TCC Ser 180	TAC Tyr	ATC Ile	TCC Ser	ATC Ile	TGC Cys 185	21	41
AAC Asn	CGC Arg	GAG Glu	ATC Ile	TCG Ser 190	CCC Pro	ACC Thr	GAG Glu	CGC Arg	TGC Cys 195	AAC Asn	CGC Arg	CGC Arg	AAG Lys	TGC Cys 200	CAC His	21	89
AAG Lys	GCC Ala	CTG Leu	CGC Arg 205	CAG Gln	TTC Phe	TTC Phe	GAC Asp	CGG Arg 210	GTG Val	CCC Pro	AGC Ser	GAG Glu	TAC Tyr 215	ACC Thr	TAC Tyr	22	37
CGC Arg	ATG Met	CTC Leu 220	TTC Phe	TGC Cys	TCC Ser	TGC Cys	CAA Gln 225	GAC Asp	CAG Gln	GCG Ala	TGC Cys	GCT Ala 230	GAG Glu	CGC Arg	CGC Arg	22	85
CGG Arg	CAA Gln 235	ACC Thr	ATC Ile	CTG Leu	CCC Pro	AGC Ser 240	TGC Cys	TCC Ser	TAT Tyr	GAG Glu	GAC Asp 245	AAG Lys	GAG Glu	AAG Lys	CCC Pro	23	33
AAC Asn 250	TGC Cys	CTG Leu	GAC Asp	CTG Leu	CGT Arg 255	GGC Gly	GTG Val	TGC Cys	CGG Arg	ACT Thr 260	GAC Asp	CAC His	CTG Leu	TGT Cys	CGG Arg 265	23	81
TCC Ser	CGG Arg	CTG Leu	GCC Ala	GAC Asp 270	TTC Phe	CAT His	GCC Ala	AAT Asn	TGT Cys 275	CGA Arg	GCC Ala	TCC Ser	TAC Tyr	CAG Gln 280	ACG Thr	24	29
GTC Val	ACC Thr	AGC Ser	TGC Cys 285	CCT Pro	GCG Ala	GAC Asp	AAT Asn	TAC Tyr 290	CAG Gln	GCG Ala	TGT Cys	CTG Leu	GGC Gly 295	TCT Ser	TAT Tyr	24	77
GCT Ala	GGC Gly	ATG Met 300	ATT Ile	GGG Gly	TTT Phe	GAC Asp	ATG Met 305	ACA Thr	CCT Pro	AAC Asn	TAT Tyr	GTG Val 310	GAC Asp	TCC Ser	AGC Ser	25	25
CCC Pro	ACT Thr	GGC Gly	ATC Ile	GTG Val	GTG Val	TCC Ser	CCC Pro	TGG Trp	TGC Cys	AGC Ser	TGT Cys	CGT Arg	GGC Gly	AGC Ser	GGG Gly	25	73

315	320	325	
AAC ATG GAG GAG GAG TGT Asn Met Glu Glu Glu Cys 330 335	GAG AAG TTC CTC AGG Glu Lys Phe Leu Arg 340	GAC TTC ACC GAG AAC Asp Phe Thr Glu Asn 345	2621
CCA TGC CTC CGG AAC GCC Pro Cys Leu Arg Asn Ala 350	ATC CAG GCC TTT GGC Ile Gln Ala Phe Gly 355	AAC GGC ACG AAC GTG Asn Gly Thr Asn Val 360	2669
AAC GTG TCC CCA AAA GGC Asn Val Ser Pro Lys Gly 365	CCC TCG TTC CAG GCC Pro Ser Phe Gln Ala 370	ACC CAG GCC CCT CGG Thr Gln Ala Pro Arg 375	2717
GTG GAG AAG ACG CCT TCT Val Glu Lys Thr Pro Ser 380	TTG CCA GAT GAC CTC Leu Pro Asp Asp Leu 385	AGT GAC AGT ACC AGC Ser Asp Ser Thr Ser 390	2765
TTG GGG ACC AGT GTC ATC Leu Gly Thr Ser Val Ile 395	ACC ACC TGC ACG TCT Thr Thr Cys Thr Ser 400	GTC CAG GAG CAG GGG Val Gln Glu Gln Gly 405	2813
CTG AAG GCC AAC AAC TCC Leu Lys Ala Asn Asn Ser 410	AAA GAG TTA AGC ATG Lys Glu Leu Ser Met 420	TGC TTC ACA GAG CTC Cys Phe Thr Glu Leu 425	2861
ACG ACA AAT ATC ATC CCA Thr Thr Asn Ile Ile Pro 430	GGG AGT AAC AAG GTG Gly Ser Asn Lys Val 435	ATC AAA CCT AAC TCA Ile Lys Pro Asn Ser 440	2909
GGC CCC AGC AGA GCC AGA Gly Pro Ser Arg Ala Arg 445	CCG TCG GCT GCC TTG Pro Ser Ala Ala Leu 450	ACC GTG CTG TCT GTC Thr Val Leu Ser Val 455	2957
CTG ATG CTG AAA CTG GCC Leu Met Leu Lys Leu Ala 460		CGAGTC AGAAGATTTT	3008
TGAAAGCTAC GCAGACAAGA AC	CAGCCGCCT GACGAAATGG	AAACACACAC AGACACACAC	3068
ACACCTTGCA AAAAAAAAT TO	STTTTTCCC ACCTTGTCGC	TGAACCTGTC TCCTCCCAGG	3128
TTTCTTCTCT GGAGAAGTTT TT	rgtaaacca aacagacaag	CAGGCAGGCA GCCTGAGAGC	3188
TGGCCCAGGG GTCCCCTGGC AG	GGGGAAACT CTGGTGCCGG	GGAGGGCACG AGGCTCTAGA	3248
AATGCCCTTC ACTTTCTCCT GO	TGTTTTTC TCTCTGGACC	CTTCTGAAGC AGAGACCGGA	3308
CAAGAGCCTG CAGCGGAAGG GA	ACTCTGGGC TGTGCCTGAG	GCTGGCTGGG GGCAGGACAA	3368
CACAGCTGCT TCCCCAGGCT GC	CCCACTCTG GGGACCCGCT	GGGGGCTGGC AGAGGGCATC	3428
GGTCAGCGGG GCAGCGGGGC TO	GCCATGAG GGTCCACCTT	CAGCCCTTTG GCTTCAAGGA	3488
TGGAGATGGT TTTGCCCTCC CT	TCTCTGCCC TCGGGTGGGG	CTGGTGGGTC TGCAGCTGGT	3548
GTGGGAACTT CCCCACGGAT GC	GCGGTGGAG GGGGTTCGCA	CCGTGCTGGG CTCCCCCTGA	3608
CTGTAGCACG GAGTGTTGGG GC	CTGGGGGCC AGCTCCAGGA	GGGCTTGAGA GCTCAGCCTG	3668
CCTGGGAGAG CCCTTGTGGC GA	AGGCATTAA AACTTGGGCA	CCAGCTTCTT TCTCGGTGGC	3728
AGAAATTTTG AAGTCAGAGA GA	AAACGGTCC TTTGTTGGCT	TCTTTGCTTT CTCGTGGGTC	3788

CTTTGGCAGG	CCTCCCTTTG	GGGAGAGGGA	GGGGAGAGAC	CACAGCCGGG	TGTGTGTCTG	3848
CAGCACCGTG	GGCCCTCAAG	CTTTCCTGCT	GTCTTCTCCC	TCCTCCTCCT	TTCCCCTTTC	3908
тстттсстса	TTTCCTAGAC	GTACGTCAAC	TGTATGTACA	TACCGGGGCT	CCTCTCCTAA	3968
CATATATGTA	TATACACATC	CATATACATA	TATTGTGTGG	TTTCCCCTTT	CTTTCCTTTT	4028
TTTAAGCAAC	AAAACTATGG	АААТААТАСС	CCAACAGATG	AGCGAAAATG	TATTATTGTA	4088
AAGTTTATTT	TTTTTAATAC	TGTTGTCTAT	AATGGGGAAA	AAGGACATTG	GCCCGCAGT	4148
GCCCTGCCCC	AGTCAGCCTG	GCTGGGCTCT	GGTGGGGGCT	CCTGATCCGC	ATCCAAGCTT	4208
AACCAAGGCT	CCAATAAACG	TGCG				4232

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 464 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ile Leu Ala Asn Val Phe Cys Leu Phe Phe Phe Leu Asp Asp Thr Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Pro Glu Leu His Gly Trp Arg Pro Pro Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr 115 Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile Phe Ser Gly Thr Gly Ala Asp Pro Val Val Ser Ala Lys Ser Asn His Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys 165 Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr 185 190

Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser Cys Gln Asp Gln Ala Cys Ala Glu Arg Arg Gln Thr Ile Leu Pro Ser 235 Cys Ser Tyr Glu Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg Gly Val Cys Arg Thr Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe His Ala Asn Cys Arg Ala Ser Tyr Gln Thr Val Thr Ser Cys Pro Ala Asp 285 280 Asn Tyr Gln Ala Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe Asp 295 Met Thr Pro Asn Tyr Val Asp Ser Ser Pro Thr Gly Ile Val Val Ser Pro Trp Cys Ser Cys Arg Gly Ser Gly Asn Met Glu Glu Cys Glu 325 330 Lys Phe Leu Arg Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala Ile Gln Ala Phe Gly Asn Gly Thr Asn Val Asn Val Ser Pro Lys Gly Pro Ser Phe Gln Ala Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu 375 Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr 395 Thr Cys Thr Ser Val Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser Lys Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile Ile Pro Gly Ser Asn Lys Val Ile Lys Pro Asn Ser Gly Pro Ser Arg Ala Arg Pro 440 Ser Ala Ala Leu Thr Val Leu Ser Val Leu Met Leu Lys Leu Ala Leu 455

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1991 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 203..1402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:												
CAAGTCAAAG GTT	TAATCAT GATCCA	AAGAG CCCAGAG	AGA CTTTAGGACA A	TAATAGGAA 60								
TAAAGCAAGG CCC	CACAGGCT CCAGCT	CCTG ATGCCCA	GAT GTTCGGCAGG A	TCCGGGGAC 120								
AGGGCAGTGC AGG	GCAGTAGT TTTCCA	ATCCT CCATCCA	GGG GAGGAGCGAG G	GGAGCGCGG 180								
AGCCCGGCGC CTACAGCTCG CC ATG GTG CGC CCC CTG AAC CCG CGA CCG CTG Met Val Arg Pro Leu Asn Pro Arg Pro Leu 1 5 10												
CCG CCC GTA GT Pro Pro Val Va	CC CTG ATG TTG al Leu Met Leu 15	CTG CTG CTG Leu Leu Leu 20	CTG CCG CCG TCG Leu Pro Pro Ser	CCG CTG 280 Pro Leu 25								
Pro Leu Ala Al	CC GGA GAC CCC a Gly Asp Pro	CTT CCC ACA Leu Pro Thr 35	GAA AGC CGA CTC Glu Ser Arg Leu 40	ATG AAC 328 Met Asn								
AGC TGT CTC CA Ser Cys Leu Gl 45	AG GCC AGG AGG n Ala Arg Arg	AAG TGC CAG Lys Cys Gln 50	GCT GAT CCC ACC Ala Asp Pro Thr 55	TGC AGT 376 Cys Ser								
GCT GCC TAC CA Ala Ala Tyr Hi 60	AC CAC CTG GAT is His Leu Asp 65	TCC TGC ACC Ser Cys Thr	TCT AGC ATA AGC Ser Ser Ile Ser 70	ACC CCA 424 Thr Pro								
CTG CCC TCA GA Leu Pro Ser Gl 75	AG GAG CCT TCG Lu Glu Pro Ser 80	GTC CCT GCT Val Pro Ala	GAC TGC CTG GAG Asp Cys Leu Glu 85	GCA GCA 472 Ala Ala 90								
CAG CAA CTC AG Gln Gln Leu Ar	GG AAC AGC TCT rg Asn Ser Ser 95	CTG ATA GGC Leu Ile Gly 100	TGC ATG TGC CAC Cys Met Cys His	CGG CGC 520 Arg Arg 105								
ATG AAG AAC CA Met Lys Asn Gl 11	ln Val Ala Cys	TTG GAC ATC Leu Asp Ile 115	TAT TGG ACC GTT Tyr Trp Thr Val 120	CAC CGT 568 His Arg								
GCC CGC AGC CT Ala Arg Ser Le 125	TT GGT AAC TAT eu Gly Asn Tyr	GAG CTG GAT Glu Leu Asp 130	GTC TCC CCC TAT Val Ser Pro Tyr 135	GAA GAC 616 Glu Asp								
ACA GTG ACC ACT Thr Val Thr Se	GC AAA CCC TGG er Lys Pro Trp 145	AAA ATG AAT Lys Met Asn	CTC AGC AAA CTG Leu Ser Lys Leu 150	AAC ATG 664 Asn Met								
CTC AAA CCA GA Leu Lys Pro As 155	AC TCA GAC CTC sp Ser Asp Leu 160	TGC CTC AAG Cys Leu Lys	TTT GCC ATG CTG Phe Ala Met Leu 165	TGT ACT 712 Cys Thr 170								
CTC AAT GAC AA Leu Asn Asp Ly	AG TGT GAC CGG ys Cys Asp Arg 175	CTG CGC AAG Leu Arg Lys 180	GCC TAC GGG GAG Ala Tyr Gly Glu	GCG TGC 760 Ala Cys 185								
Ser Gly Pro Hi	AC TGC CAG CGC is Cys Gln Arg	CAC GTC TGC His Val Cys 195	CTC AGG CAG CTG Leu Arg Gln Leu 200	CTC ACT 808 Leu Thr								

TTC TTC GAG AAG GCC GCC GAG CCC CAC GCG CAG GGC CTG CTA CTG TGC Phe Phe Glu Lys Ala Ala Glu Pro His Ala Gln Gly Leu Leu Cys 205 210 215	856
CCA TGT GCC CCC AAC GAC CGG GGC TGC GGG GAG CGC CGG CGC AAC ACC Pro Cys Ala Pro Asn Asp Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr 220 230	904
ATC GCC CCC AAC TGC GCG CTG CCG CCT GTG GCC CCC AAC TGC CTG GAG Ile Ala Pro Asn Cys Ala Leu Pro Pro Val Ala Pro Asn Cys Leu Glu 235 240 245 250	952
CTG CGG CGC CTC TGC TTC TCC GAC CCG CTT TGC AGA TCA CGC CTG GTG Leu Arg Arg Leu Cys Phe Ser Asp Pro Leu Cys Arg Ser Arg Leu Val 255 260 265	1000
GAT TTC CAG ACC CAC TGC CAT CCC ATG GAC ATC CTA GGA ACT TGT GCA Asp Phe Gln Thr His Cys His Pro Met Asp Ile Leu Gly Thr Cys Ala 270 275 280	1048
ACA GAG CAG TCC AGA TGT CTA CGA GCA TAC CTG GGG CTG ATT GGG ACT Thr Glu Gln Ser Arg Cys Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr 285 290 295	1096
GCC ATG ACC CCC AAC TTT GCC AGC AAT GTC AAC ACC AGT GTT GCC TTA Ala Met Thr Pro Asn Phe Ala Ser Asn Val Asn Thr Ser Val Ala Leu 300 305 310	1144
AGC TGC ACC TGC CGA GGC AGT GGC AAC CTG CAG GAG GAG TGT GAA ATG Ser Cys Thr Cys Arg Gly Ser Gly Asn Leu Gln Glu Glu Cys Glu Met 315	1192
CTG GAA GGG TTC TTC TCC CAC AAC CCC TGC CTC ACG GAG GCC ATT GCA Leu Glu Gly Phe Phe Ser His Asn Pro Cys Leu Thr Glu Ala Ile Ala 335 340 345	1240
GCT AAG ATG CGT TTT CAC AGC CAA CTC TTC TCC CAG GAC TGG CCA CAC Ala Lys Met Arg Phe His Ser Gln Leu Phe Ser Gln Asp Trp Pro His 350 355	1288
CCT ACC TTT GCT GTG ATG GCA CAC CAG AAT GAA AAC CCT GCT GTG AGG Pro Thr Phe Ala Val Met Ala His Gln Asn Glu Asn Pro Ala Val Arg 365 370 375	1336
CCA CAG CCC TGG GTG CCC TCT CTT TTC TCC TGC ACG CTT CCC TTG ATT Pro Gln Pro Trp Val Pro Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile 380 385 390	1384
CTG CTC CTG AGC CTA TGG TAGCTGGACT TCCCCAGGGC CCTCTTCCCC Leu Leu Ser Leu Trp 395 400	1432
TCCACCACAC CCAGGTGGAC TTGCAGCCCA CAAGGGGTGA GGAAAGGACA GCAGCAGGAA	1492
GGAGGTGCAG TGCGCAGATG AGGGCACAGG AGAAGCTAAG GGTTATGACC TCCAGATCCT	1552
TACTGGTCCA GTCCTCATTC CCTCCACCC ATCTCCACTT CTGATTCATG CTGCCCCTCC	1612
TTGGTGGCCA CAATTTAGCC ATGTCATCTG GTGGTGACCA GCTCCACCAA GCCCCTTTGT	1672
GAGCCCTTCC TCTTGACTAC CAGGATCACC AGAATCTAAT AAGTTAGCCT TTCTCTATTG	1732
CATTCCAGAT TAGGGTTAGG GTAGGGAGGA CTGGGTGTTC TGAGGCAGCC TAGAAAGTCA	1792

TTCTCCTTTG	TGAAGAAGGC	TCCTGCCCCC	TCGTCTCCTC	CTCTGAGTGG	AGGATGGAAA	1852
ACTACTGCCT	GCACTGCCCT	GTCCCCGGAT	CCTGCCGAAC	ATCTGGGCAT	CAGGAGCTGG	1912
AGCCTGTGGG	CCTTGCTTTA	TTCCTATTAT	TGTCCTAAAG	TCTCTCTGGG	CTCTTGGATC	1972
ATGATTAAAC	CTTTGACTG					1991

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 400 amino acids

 (B) TYPE: amino acid

 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

	(2	(i) :	SEQUE	ENCE	DESC	CRIPT	ON:	SEÇ	O ID	NO:3	88:				
Met 1	Val	Arg	Pro	Leu 5	Asn	Pro	Arg	Pro	Leu 10	Pro	Pro	Val	Val	Leu 15	Met
Leu	Leu	Leu	Leu 20	Leu	Pro	Pro	Ser	Pro 25	Leu	Pro	Leu	Ala	Ala 30	Gly	Asp
Pro	Leu	Pro 35	Thr	Glu	Ser	Arg	Leu 40	Met	Asn	Ser	Cys	Leu 45	Gln	Ala	Arg
Arg	Lys 50	Cys	Gln	Ala	Asp	Pro 55	Thr	Cys	Ser	Ala	Ala 60	Tyr	His	His	Leu
Asp 65	Ser	Cys	Thr	Ser	Ser 70	Ile	Ser	Thr	Pro	Leu 75	Pro	Ser	Glu	Glu	Pro 80
Ser	Val	Pro	Ala	Asp 85	Cys	Leu	Glu	Ala	Ala 90	Gln	Gln	Leu	Arg	Asn 95	Ser
Ser	Leu	Ile	Gly 100	Cys	Met	Cys	His	Arg 105	Arg	Met	Lys	Asn	Gln 110	Val	Ala
Cys	Leu	Asp 115	Ile	Tyr	Trp	Thr	Val 120	His	Arg	Ala	Arg	Ser 125	Leu	Gly	Asn
Tyr	Glu 130	Leu	Asp	Val	Ser	Pro 135	Tyr	Glu	Asp	Thr	Val 140	Thr	Ser	Lys	Pro
Trp 145	Lys	Met	Asn	Leu	Ser 150	Lys	Leu	Asn	Met	Leu 155	Lys	Pro	Asp	Ser	Asp 160
Leu	Cys	Leu	Lys	Phe 165	Ala	Met	Leu	Cys	Thr 170	Leu	Asn	Asp	Lys	Cys 175	Asp
Arg	Leu	Arg	Lys 180	Ala	Tyr	Gly	Glu	Ala 185	Суз	Ser	Gly	Pro	His 190	Cys	Gln
Arg	His	Val 195	Cys	Leu	Arg	Gln	Leu 200	Leu	Thr	Phe	Phe	Glu 205	Lys	Ala	Ala
Glu	Pro 210	His	Ala	Gln	Gly	Leu 215	Leu	Leu	Сув	Pro	Cys 220	Ala	Pro	Asn	Asp
Arg	Gly	Суѕ	Gly	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala

225					230					235					240	
Leu	Pro	Pro	Val	Ala 245	Pro	Asn	Cys	Leu	Glu 250	Leu	Arg	Arg	Leu	Cys 255	Phe	
Ser	Asp	Pro	Leu 260	Cys	Arg	Ser	Arg	Leu 265	Val	Asp	Phe	Gln	Thr 270	His	Cys	
His	Pro	Met 275	Asp	Ile	Leu	Gly	Thr 280	Cys	Ala	Thr	Glu	Gln 285	Ser	Arg	Cys	
Leu	Arg 290	Ala	Tyr	Leu	Gly	Leu 295	Ile	Gly	Thr	Ala	Met 300	Thr	Pro	Asn	Phe	
Ala 305	Ser	Asn	Val	Asn	Thr 310	Ser	Val	Ala	Leu	Ser 315	Cys	Thr	Cys	Arg	Gly 320	
Ser	Gly	Asn	Leu	Gln 325	Glu	Glu	Суѕ	Glu	Met 330	Leu	Glu	Gly	Phe	Phe 335	Ser	
His	Asn	Pro	Cys 340	Leu	Thr	Glu	Ala	Ile 345	Ala	Ala	Lys	Met	Arg 350	Phe	His .	
Ser	Gln	Leu 355	Phe	Ser	Gln	Asp	Trp 360	Pro	His	Pro	Thr	Phe 365	Ala	Val	Met	
Ala	His 370	Gln	Asn	Glu	Asn	Pro 375	Ala	Val	Arg	Pro	Gln 380	Pro	Trp	Val	Pro	
Ser 385	Leu	Phe	Ser	Cys	Thr 390	Leu	Pro	Leu	Ile	Leu 395	Leu	Leu	Ser	Leu	Trp 400	
(2)	INFO	ORMA'	rion	FOR	SEQ	ID I	NO: 39	9:								
	(i)	(2 (1 (0	A) L1 B) T' C) S'	ENGTI YPE: TRANI	HARAG H: 22 nuc: DEDNI DGY:	215 l leic ESS:	oase acio sino	pai: i	rs							
	(ii)) MO	LECU!	LE T	YPE:	cDN	A									
	(ix)	(2		AME/	KEY: ION:		20	63								
	(xi)) SE	QUEN	CE D	ESCR:	IPTI	ON:	SEQ :	ID N	0:39	:					
GCG	GCCG	CGT (CGAC	CTTG	AC C	ATGC	AGAC	A CT	rttt(CAGG	CCT	CTGT	CTG (GTGT	GAAGTT	+

GCGGCCGCGT CGACCTTGAC CATGCAGACA CTTTTTCAGG CCTCTGTCTG GTGTGAAGTT 60

GGCAGATACA AGCAAGGCCC GAAAGGGGTC TCAGCTTCTC TCTCCTGGGC CTCCTGGACT 120

GAGTTAGGCT TGCTTCTGGT TGTCTTCTAA AGGCACGGTG ATACAGAATG ATGAGACTAG 180

GCTGGAGGGG GCTTTCTGCT TCTCTGTGTG TGACCTTGAG TTATCTCCCT TCGTTGGATC 240

CGAGCTTTCC TGGAATATGA TGTTGAATAT GAATATGAGT TCTGCCTAAG GTCCAGACAG 300

GCTCTGAGGG TTAACTGACT TTTGGAGCCT TCAAATCAAT ACCTTGGATG GAGTGGGGGT 360

TTGTCCAATG GGAGTTGAGG CAAGATCCCT TTGCATAAGC CTTGCCACAT CATGTTGAAG 420

CCATGCCATT CTGTCTGGAC TATTGGCATC TTACCTTTCC AGCAGTTTCA GTGAAGGCCT	480
TCCTGGATTT ATCATTCTGT GTTCCACTGC CTAGGATTGT GCTCAAGAGG AAATGAATGT	540
GAACCATGGT TGTAGGGGAG TATGGCCAAC CAGGTTGGGT CTGTGTTGAC CTTGGTCTTG	600
GTGTTCTTTT GTGTAAAGTG GGTGAGAAGT TCCTTCAAAC CTTAGGCCTA CATTGGGGTC	660
AGAGACTGTG GTGGCCCTCA TTC ATG CTT GTC TTC CCT TCC CAC TAC CCA Met Leu Val Phe Pro Ser His Tyr Pro 1 5	710
GAC GAA ACC CTC CGC TCT TTG GCC AGC CCT TCC TCC CTG CAG GGC TCT Asp Glu Thr Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Ser 10 20 25	758
GAG CTC CAC GGC TGG CGC CCC CAA GTG GAC TGT GTC CGG GCC AAT GAG Glu Leu His Gly Trp Arg Pro Gln Val Asp Cys Val Arg Ala Asn Glu 30 35 40	806
CTG TGT GCG GCT GAA TCC AAC TGC AGC TCC AGG TAC CGC ACC CTT CGG Leu Cys Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg 45	854
CAG TGC CTG GCA GGC CGG GAT CGC AAT ACC ATG CTG GCC AAT AAG GAG Gln Cys Leu Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu 60 65 70	902
TGC CAG GCA GCC CTG GAG GTC TTG CAG GAA AGC CCA CTG TAT GAC TGC Cys Gln Ala Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys 75 80 85	950
CGC TGC AAG CGG GGC ATG AAG AAG GAG CTG CAG TGT CTG CAG ATC TAC Arg Cys Lys Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr 90 95 100 105	998
TGG AGC ATC CAT CTG GGG CTG ACA GAG GGT GAG GAG TTC TAT GAA GCT Trp Ser Ile His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala 110 115 120	1046
TCC CCC TAT GAG CCT GTG ACC TCG CGC CTC TCG GAC ATC TTC AGG CTC Ser Pro Tyr Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu 125	1094
GCT TCA ATC TTC TCA GGG ACA GGG ACA GAC CCG GCG GTC AGT ACC AAA Ala Ser Ile Phe Ser Gly Thr Gly Thr Asp Pro Ala Val Ser Thr Lys 140 145 150	1142
AGC AAC CAC TGC CTG GAT GCC GCC AAG GCC TGC AAC CTG AAT GAC AAC Ser Asn His Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn 155 160 165	1190
TGC AAG AAG CTT CGC TCC TCT TAT ATC TCC ATC TGC AAC CGT GAG ATC Cys Lys Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile 170 175 180 185	1238
TCT CCC ACC GAA CGC TGC AAC CGC CGC AAG TGC CAC AAG GCT CTG CGC Ser Pro Thr Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg 190 195 200	1286
CAG TTC TTT GAC CGT GTG CCC AGC GAG TAT ACC TAC CGC ATG CTC TTC Gln Phe Phe Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe 205 210 215	1334

TGC Cys	TCC Ser	TGT Cys 220	CAG Gln	GAC Asp	CAG Gln	GCA Ala	TGT Cys 225	GCT Ala	GAG Glu	CGT Arg	CGC Arg	CGG Arg 230	CAA Gln	ACC Thr	ATC Ile	1:	382
CTG Leu	CCC Pro 235	AGT Ser	TGC Cys	TCC Ser	TAT Tyr	GAG Glu 240	GAC Asp	AAG Lys	GAG Glu	AAG Lys	CCC Pro 245	AAC Asn	TGC Cys	CTG Leu	GAC Asp	1	430
CTG Leu 250	CGC Arg	AGC Ser	CTG Leu	TGT Cys	CGT Arg 255	ACA Thr	GAC Asp	CAC His	CTG Leu	TGC Cys 260	CGG Arg	TCC Ser	CGA Arg	CTG Leu	GCA Ala 265	1	478
GAT Asp	TTC Phe	CAC His	GCC Ala	AAC Asn 270	TGT Cys	CGA Arg	GCC Ala	TCC Ser	TAC Tyr 275	CGG Arg	ACA Thr	ATC Ile	ACC Thr	AGC Ser 280	TGT Cys	1!	526
CCT Pro	GCG Ala	GAC Asp	AAC Asn 285	TAC Tyr	CAG Gln	GCA Ala	TGT Cys	CTG Leu 290	GGC Gly	TCC Ser	TAT Tyr	GCT Ala	GGC Gly 295	ATG Met	ATT Ile	1	574
GGG Gly	TTT Phe	GAT Asp 300	ATG Met	ACA Thr	CCC Pro	AAC Asn	TAT Tyr 305	GTG Val	GAC Asp	TCC Ser	AAC Asn	CCC Pro 310	ACG Thr	GGC Gly	ATC Ile	10	622
GTG Val	GTG Val 315	TCT Ser	CCC Pro	TGG Trp	TGC Cys	AAT Asn 320	TGT Cys	CGT Arg	GGC Gly	AGT Ser	GGG Gly 325	AAC Asn	ATG Met	GAA Glu	GAA Glu	10	670
GAG Glu 330	TGT Cys	GAG Glu	AAG Lys	TTC Phe	CTC Leu 335	AGG Arg	GAC Asp	TTC Phe	ACG Thr	GAA Glu 340	AAC Asn	CCA Pro	TGC Cys	CTC Leu	CGG Arg 345	1'	718
AAT Asn	GCC Ala	ATT Ile	CAG Gln	GCC Ala 350	TTT Phe	GGT Gly	AAT Asn	GGC Gly	ACA Thr 355	GAT Asp	GTG Val	AAC Asn	ATG Met	TCT Ser 360	CCC Pro	1	766
AAA Lys	GGC Gly	CCC Pro	TCA Ser 365	CTC Leu	CCA Pro	GCT Ala	ACC Thr	CAG Gln 370	GCC Ala	CCT Pro	CGG Arg	GTG Val	GAG Glu 375	AAG Lys	ACT Thr	1:	814
CCT Pro	TCA Ser	CTG Leu 380	CCA Pro	GAT Asp	GAC Asp	CTC Leu	AGT Ser 385	GAC Asp	AGC Ser	ACC Thr	AGC Ser	CTG Leu 390	GGG Gly	ACC Thr	AGT Ser	1:	862
GTC Val	ATC Ile 395	ACC Thr	ACC Thr	TGC Cys	ACA Thr	TCT Ser 400	ATC Ile	CAG Gln	GAG Glu	CAA Gln	GGG Gly 405	CTG Leu	AAG Lys	GCC Ala	AAC Asn	19	910
AAC Asn 410	TCC Ser	AAA Lys	GAG Glu	TTA Leu	AGC Ser 415	ATG Met	TGC Cys	TTC Phe	ACA Thr	GAG Glu 420	CTC Leu	ACG Thr	ACA Thr	AAC Asn	ATC Ile 425	19	958
AGT Ser	CCA Pro	GGG Gly	AGT Ser	AAA Lys 430	AAG Lys	GTG Val	ATC Ile	AAA Lys	CTT Leu 435	AAC Asn	TCA Ser	GGC Gly	TCC Ser	AGC Ser 440	AGA Arg	2	006
GCC Ala	AGA Arg	CTG Leu	TCG Ser 445	GCT Ala	GCC Ala	TTG Leu	ACT Thr	GCC Ala 450	CTC Leu	CCA Pro	CTC Leu	CTG Leu	ATG Met 455	CTG Leu	ACC Thr	2	054
	GCC Ala			GCCT'	rtg (GAAC	CCAG	CA C	AAAA(TTC:	r TC	AAGC	AACC			2	103

2163

2215

CAGATATGAA CTCCCGCCTG ACAAAATGGA AACACACGCA TACACACATG CCACACACAG ACACACAC AGACACACA ACACACAC ATACAGACGT CGACGCGGCC GC (2) INFORMATION FOR SEQ ID NO:40: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 460 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40: Met Leu Val Phe Pro Ser His Tyr Pro Asp Glu Thr Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Ser Glu Leu His Gly Trp Arg Pro Gln Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile Phe Ser Gly Thr Gly Thr Asp Pro Ala Val Ser Thr Lys Ser Asn His Cys Leu Asp Ala 150 Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Arg Val Pro 200 Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser Cys Gln Asp Gln Ala 215 Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro Ser Cys Ser Tyr Glu

Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg Ser Leu Cys Arg Thr

250

Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe His Ala Asn Cys Arg Ala Ser Tyr Arg Thr Ile Thr Ser Cys Pro Ala Asp Asn Tyr Gln Ala 280 Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe Asp Met Thr Pro Asn Tyr Val Asp Ser Asn Pro Thr Gly Ile Val Val Ser Pro Trp Cys Asn 315 Cys Arg Gly Ser Gly Asn Met Glu Glu Glu Cys Glu Lys Phe Leu Arg 330 Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala Ile Gln Ala Phe Gly Asn Gly Thr Asp Val Asn Met Ser Pro Lys Gly Pro Ser Leu Pro Ala 360 Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr Thr Cys Thr Ser Ile Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser Lys Glu Leu Ser Met 405 410 Cys Phe Thr Glu Leu Thr Thr Asn Ile Ser Pro Gly Ser Lys Lys Val Ile Lys Leu Asn Ser Gly Ser Ser Arg Ala Arg Leu Ser Ala Ala Leu 440 Thr Ala Leu Pro Leu Leu Met Leu Thr Leu Ala Leu 455 450

- (2) INFORMATION FOR SEQ ID NO:41:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1699 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 67..1257
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCGGCCGCGT CGACCGACGC CCAGCACAGG CAGAGCGCTG CCGGGTCCGC GGCGTCCAGA 60

CCCGCC ATG GGG CTC TCC CGG AGC CCG CGA CCG CCG CCG CTA GTG ATC

Met Gly Leu Ser Arg Ser Pro Arg Pro Pro Pro Leu Val Ile

1 5 10

CTG Leu 15	CTA Leu	CTG Leu	GTG Val	CTG Leu	TCG Ser 20	CTG Leu	TGG Trp	CTA Leu	CCC Pro	CTT Leu 25	GGA Gly	ACA Thr	GGA Gly	AAC Asn	TCC Ser 30	156
CTT Leu	CCC Pro	ACA Thr	GAG Glu	AAC Asn 35	AGG Arg	CTT Leu	GTG Val	AAC Asn	AGC Ser 40	TGT Cys	ACC Thr	CAG Gln	GCC Ala	AGA Arg 45	AAA Lys	204
AAA Lys	TGC Cys	GAG Glu	GCT Ala 50	AAT Asn	CCC Pro	GCT Ala	TGC Cys	AAG Lys 55	GCT Ala	GCC Ala	TAC Tyr	CAG Gln	CAC His 60	CTG Leu	GAC Asp	252
TCC Ser	TGC Cys	ACC Thr 65	CCC Pro	AGT Ser	CTC Leu	AGC Ser	AGT Ser 70	CCA Pro	CTG Leu	CCC Pro	TCA Ser	GGG Gly 75	GAG Glu	TCT Ser	GCC Ala	300
ACA Thr	TCT Ser 80	GCA Ala	GCG Ala	TGC Cys	CTT Leu	GAA Glu 85	GCA Ala	GCA Ala	CAG Gln	CAA Gln	CTC Leu 90	AGG Arg	AAC Asn	AGC Ser	TCT Ser	348
CTC Leu 95	ATA Ile	GAC Asp	TGC Cys	AGG Arg	TGC Cys 100	CAC His	CGG Arg	CGC Arg	ATG Met	AAG Lys 105	CAC His	CAA Gln	GCT Ala	ACC Thr	TGT Cys 110	396
CTG Leu	GAC Asp	ATT Ile	TAT Tyr	TGG Trp 115	ACC Thr	GTT Val	CAC His	CCT Pro	GTC Val 120	CGA Arg	AGC Ser	CTT Leu	GGT Gly	GAC Asp 125	TAC Tyr	444
GAG Glu	TTG Leu	GAC Asp	GTC Val 130	TCA Ser	CCC Pro	TAT Tyr	GAA Glu	GAC Asp 135	ACA Thr	GTG Val	ACC Thr	AGC Ser	AAA Lys 140	CCC Pro	TGG Trp	492
AAA Lys	ATG Met	AAT Asn 145	CTC Leu	AGC Ser	AAG Lys	CTG Leu	AGC Ser 150	ATG Met	CTC Leu	AAA Lys	CCA Pro	GAC Asp 155	TCC Ser	GAC Asp	CTC Leu	540
TGC Cys	CTC Leu 160	AAA Lys	TTT Phe	GCT Ala	ATG Met	CTG Leu 165	TGT Cys	ACT Thr	CTT Leu	AAC Asn	GAC Asp 170	AAG Lys	TGC Cys	GAC Asp	CGC Arg	588
CTC Leu 175	CGA Arg	AAG Lys	GCC Ala	TAC Tyr	GGG Gly 180	GAG Glu	GCG Ala	TGC Cys	TCA Ser	GGG Gly 185	ATC Ile	CGC Arg	TGC Cys	CAG Gln	CGC Arg 190	636
CAC His	CTC Leu	TGC Cys	CTA Leu	GCT Ala 195	CAG Gln	CTG Leu	CGC Arg	TCC Ser	TTC Phe 200	TTC Phe	GAG Glu	AAG Lys	GCG Ala	GCA Ala 205	GAG Glu	684
TCC Ser	CAC His	GCT Ala	CAG Gln 210	GGC Gly	CTG Leu	CTG Leu	CTG Leu	TGT Cys 215	CCC Pro	TGT Cys	GCA Ala	CCC Pro	GAA Glu 220	GAT Asp	GCG Ala	732
GGC Gly	TGT Cys	GGG Gly 225	GAG Glu	CGC Arg	CGG Arg	CGC Arg	AAC Asn 230	ACC Thr	ATC Ile	GCC Ala	CCC Pro	AGT Ser 235	TGC Cys	GCC Ala	CTC Leu	780
CCG Pro	TCT Ser 240	GTG Val	GCC Ala	CCC Pro	AAC Asn	TGC Cys 245	CTA Leu	GAT Asp	CTT Leu	CGG Arg	AGC Ser 250	TTC Phe	TGC Cys	CGT Arg	GCG Ala	828
GAC Asp 255	CCT Pro	CTG Leu	TGC Cys	AGA Arg	TCA Ser 260	CGC Arg	CTG Leu	ATG Met	GAC Asp	TTC Phe 265	CAG Gln	ACC Thr	CAC His	TGC Cys	CAC His 270	876

CCT Pro	ATG Met	GAC Asp	ATC Ile	CTC Leu 275	GGG Gly	ACT Thr	TGT Cys	GCA Ala	ACT Thr 280	GAG Glu	CAG Gln	TCC Ser	AGA Arg	TGT Cys 285	CTG Leu	924
CGG Arg	GCA Ala	TAC Tyr	CTG Leu 290	GGG Gly	CTA Leu	ATT Ile	GGG Gly	ACT Thr 295	GCC Ala	ATG Met	ACC Thr	CCA Pro	AAC Asn 300	TTC Phe	ATC Ile	972
AGC Ser	AAG Lys	GTC Val 305	AAC Asn	ACT Thr	ACT Thr	GTT Val	GCC Ala 310	TTA Leu	GGC Gly	TGT Cys	ACC Thr	TGC Cys 315	CGA Arg	GGC Gly	AGT Ser	1020
GGC Gly	AAC Asn 320	CTG Leu	CAG Gln	GAC Asp	GAG Glu	TGT Cys 325	GAA Glu	CAG Gln	CTG Leu	GAA Glu	AAG Lys 330	TCC Ser	TTC Phe	TCC Ser	CAG Gln	1068
AAC Asn 335	CCC Pro	TGC Cys	CTC Leu	ATG Met	GAG Glu 340	GCC Ala	ATT Ile	GCG Ala	GCT Ala	AAA Lys 345	ATG Met	CGT Arg	TTC Phe	CAC His	AGA Arg 350	1116
CAA Gln	CTC Leu	TTC Phe	TCC Ser	CAG Gln 355	GAC Asp	TGG Trp	GCG Ala	GAC Asp	TCT Ser 360	ACT Thr	TTT Phe	TCT Ser	GTG Val	ATG Met 365	CAG Gln	1164
CAG Gln	CAG Gln	AAC Asn	AGC Ser 370	AGC Ser	CCT Pro	GCT Ala	CTG Leu	AGG Arg 375	CCC Pro	CAG Gln	CTC Leu	AGG Arg	CTA Leu 380	CCC Pro	GTT Val	1212
CTG Leu	TCT Ser	TTC Phe 385	TTC Phe	ATC Ile	CTT Leu	ACC Thr	TTG Leu 390	ATT Ile	CTG Leu	CTG Leu	CAG Gln	ACC Thr 395	CTC Leu	TGG Trp		1257
TAAC	TGGG	CT (CCTC	CAGGG	T CC	TTTC	TCCI	CTC	CACC	CACA	CCC	GACC	CGA (CTTGC	CAGCCT	1317
GTG	TGGG	GAG A	AGAAZ	ATGO	T GO	CCTC	TGGA	A AGA	AAGAT	GCA	ACCA	GGCI	CA (CTGC	CATCC	1377
TGTC	TGCT	CC A	AGATO	BAGGT	т Э	GGAZ	GAAG	G CG	AGGGC	TGT	GACC	GTTC	CAG A	AATCO	CTGAGC	1437
GGC	CAGCT	TTT C	CAAAC	CTCT	C CI	PACTI	ACTO	CTC	CTTC	GGC	TGCT	CCTC	CC T	ragg <i>i</i>	ACCTTG	1497
TACI	CCAG	TT T	rggci	rgtai	TA TI	GTGC	STGGT	GAT	TAGO	TTC	CCAC	CTCC	CAG (CCCTI	CTTCC	1557
TGTT	TCCC	CAG (GACCA	ACCC	AG GG	CTA	ATGAC	TC	ACTCA	TTC	CTGG	TTGC	CT :	гстсс	CAGGAA	1617
GGC	AGGCT	GA (GGGTT	CTG	AG GC	CAGCI	GAGA	AAC	SATGO	TCC	СТТТ	GTG	AGG A	AAGGC	CTGGTG	1677
GTCC	CAACC	CGT (CGAC	GCGGC	CC GC	:										1699

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 397 amino acids

 - (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Gly Leu Ser Arg Ser Pro Arg Pro Pro Pro Leu Val Ile Leu Leu 1 5 10 15

Leu Val Leu Ser Leu Trp Leu Pro Leu Gly Thr Gly Asn Ser Leu Pro

25 20 Thr Glu Asn Arg Leu Val Asn Ser Cys Thr Gln Ala Arg Lys Lys Cys Glu Ala Asn Pro Ala Cys Lys Ala Ala Tyr Gln His Leu Asp Ser Cys Thr Pro Ser Leu Ser Ser Pro Leu Pro Ser Gly Glu Ser Ala Thr Ser Ala Ala Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser Ser Leu Ile Asp Cys Arg Cys His Arg Arg Met Lys His Gln Ala Thr Cys Leu Asp 105 Ile Tyr Trp Thr Val His Pro Val Arg Ser Leu Gly Asp Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro Trp Lys Met Asn Leu Ser Lys Leu Ser Met Leu Lys Pro Asp Ser Asp Leu Cys Leu 155 150 Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Ile Arg Cys Gln Arg His Leu Cys Leu Ala Gln Leu Arg Ser Phe Phe Glu Lys Ala Ala Glu Ser His 200 Ala Gln Gly Leu Leu Cys Pro Cys Ala Pro Glu Asp Ala Gly Cys 220 Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Ser Cys Ala Leu Pro Ser Val Ala Pro Asn Cys Leu Asp Leu Arg Ser Phe Cys Arg Ala Asp Pro 250 Leu Cys Arg Ser Arg Leu Met Asp Phe Gln Thr His Cys His Pro Met 265 Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe Ile Ser Lys 300 Val Asn Thr Thr Val Ala Leu Gly Cys Thr Cys Arg Gly Ser Gly Asn 310 Leu Gln Asp Glu Cys Glu Gln Leu Glu Lys Ser Phe Ser Gln Asn Pro Cys Leu Met Glu Ala Ile Ala Ala Lys Met Arg Phe His Arg Gln Leu Phe Ser Gln Asp Trp Ala Asp Ser Thr Phe Ser Val Met Gln Gln 360

Asn Ser Ser Pro Ala Leu Arg Pro Gln Leu Arg Leu Pro Val Leu Ser

Phe Phe Ile Leu Thr Leu Ile Leu Leu Gln Thr Leu Trp

- (2) INFORMATION FOR SEQ ID NO:43:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 amino acids (B) TYPE: amino acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Val Xaa Xaa Leu Xaa Xaa Xaa Pro Xaa Pro Pro Xaa Xaa Xaa Met Xaa Leu Xaa Leu Leu Ser Leu Ala Leu Pro Leu Xaa Xaa Xaa Leu Gln Gly Ala Glu Leu Xaa Gly Xaa Xaa Arg Leu Xaa Xaa Asp Cys Val Xaa Ala Xaa Xaa Xaa Cys Xaa Ala Glu Xaa Xaa Cys Ser Xaa Xaa Tyr Arg Thr Leu Arg Gln Cys Xaa Ala Gly Xaa Xaa Xaa Asn Thr Xaa Leu Ala Ser Gly Xaa Glu Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Ala Xaa Glu Xaa Leu Xaa Xaa Ser Ser Leu Tyr Asp Cys Arg Cys Lys Arg Gly Met Lys Lys Glu Xaa Xaa Cys Leu Xaa Ile Tyr Trp Ser Xaa His Xaa Xaa Leu Xaa Xaa Gly Asn Xaa Xaa Leu Glu Xaa Ser Pro Tyr Glu Pro Xaa 135 Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Xaa Xaa Ser Xaa Xaa Ser 150 Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Lys Ser Asn Xaa Cys Leu 170 Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Xaa Cys Lys Leu Arg

Ser Ala Tyr Ile Xaa Xaa Cys Xaa Xaa Xaa Ser Xaa Xaa Glu Arg

Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys

Val Pro Xaa Xaa His Xaa Tyr Gly Met Leu Phe Cys Ser Cys Xaa Xaa Xaa Asp Xaa Ala Cys Xaa Glu Arg Arg Arg Gln Thr Ile Xaa Pro Ser Cys Ser Tyr Glu Xaa Xaa Glu Lys Pro Asn Cys Leu Asp Leu Arg Xaa Xaa Cys Arg Thr Asp Xaa Leu Cys Arg Ser Arg Leu Ala Asp Phe Xaa Thr Asn Cys Xaa Xaa Xaa Xaa Arg Xaa Val Xaa Ser Cys Xaa Ala Xaa Asn Tyr Xaa Xaa Cys Leu Xaa Ala Tyr Xaa Gly Leu Ile Gly Thr Xaa Met Thr Pro Asn Tyr Val Asp Ser Ser Xaa Thr Xaa Xaa Xaa Val Ala Pro Trp Cys Xaa Cys Arg Gly Ser Gly Asn Xaa Xaa Glu Glu Cys Glu Lys Phe Leu Xaa Phe Phe Xaa Xaa Asn Pro Cys Leu Xaa Asn Ala Ile Xaa Pro Xaa Phe Ser Val Xaa Xaa Xaa Xaa Thr Xaa Thr Xaa Ala Xaa Arg Val Xaa Xaa Xaa Pro Ser Leu Xaa Xaa Xaa Xaa Ser Xaa Xaa 410 Xaa Xaa Leu Xaa Thr Xaa Val Xaa Xaa Xaa Cys Xaa Xaa Leu Gln Xaa 425 Gln Xaa Leu Lys Xaa Asn Xaa Ser Xaa Glu Xaa Xaa Xaa Cys Phe Xaa 440 Glu Leu Thr Thr Asn Xaa Xaa Xaa Ser Gly Xaa Xaa Xaa Ile 455 Xaa Xaa Xaa Ser Xaa Xaa Ala Xaa Pro Ser Xaa Ala Leu Xaa Xaa Leu Pro Val Leu Met Leu Thr Ala Leu Ala Xaa Leu Leu Ser Xaa Xaa Xaa 490 485 Xaa Ser

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 489 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

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(xi)			E DES												
Xaa 1	Xaa	Xaa	Xaa	Xaa 5	Xaa	Xaa	Xaa	Xaa	Pro 10	Xaa	Xaa	Xaa	Xaa	Leu 15	Xaa
Thr	Leu	Xaa	Ser 20	Leu	Xaa	Xaa	Pro	Leu 25	Xaa	Leu	Xaa	Xaa	Ser 30	Xaa	Xaa
Xaa	Xaa	Xaa 35	Arg	Xaa	Xaa	Xaa	Asp 40	Cys	Val	Xaa	Ala	Xaa 45	Xaa	Xaa	Cys
Xaa	Ala 50	Glu	Xaa	Xaa	Cys	Ser 55	Xaa	Xaa	Tyr	Arg	Thr 60	Leu	Arg	Gln	Cys
Xaa 65	Ala	Gly	Xaa	Xaa	Xaa 70	Asn	Xaa	Xaa	Xaa	Xaa 75	Xaa	Xaa	Xaa	Xaa	Ala 80
Xaa	Xaa	Glu	Cys	Xaa 85	Xaa	Ala	Xaa	Glu	Xaa 90	Leu	Xaa	Xaa	Ser	Ser 95	Leu
Туr	Asp	Cys	Arg 100	Cys	Lys	Arg	Gly	Met 105	Lys	Lys	Glu	Xaa	Xaa 110	Cys	Leu
Xaa	Ile	Tyr 115	Trp	Ser	Xaa	His	Xaa 120	Xaa	Leu	Xaa	Xaa	Gly 125	Xaa	Xaa	Xaa
Leu	Glu 130	Xaa	Ser	Pro	Tyr	Glu 135	Xaa	Pro	Val	Thr	Ser 140	Arg	Leu	Ser	Asp
Ile 145	Phe	Arg	Xaa	Xaa	Ser 150	Xaa	Xaa	Ser	Xaa	Xaa 155	Xaa	Xaa	Asp	Xaa	Xaa 160
Xaa	Xaa	Xaa	Lys	Ser 165	Asn	Xaa	Cys	Leu	Asp 170	Ala	Ala	Lys	Ala	Cys 175	Asn
Leu	Asn	Asp	Xaa 180	Cys	Lys	Lys	Leu	Arg 185	Ser	Ala	Tyr	Ile	Xaa 190	Xaa	Cys
Xaa	Xaa	Xaa 195	Xaa	Ser	Xaa	Xaa	Glu 200	Arg	Cys	Asn	Arg	Arg 205	Lys	Cys	His
Lys	Ala 210	Leu	Arg	Gln	Phe	Phe 215	Asp	Lys	Val	Pro	Xaa 220	Xaa	His	Xaa	Tyr
Gly 225	Met	Leu	Phe	Cys	Ser 230	Cys	Xaa	Xaa	Xaa	Asp 235	Xaa	Ala	Суѕ	Xaa	Glu 240
Arg	Arg	Arg	Gln	Thr 245	Ile	Xaa	Pro	Ser	Cys 250	Ser	Tyr	Glu	Xaa	Xaa 255	Glu
Xaa	Pro	Asn	Cys 260	Leu	Asp	Leu	Arg	Ser 265	Xaa	Cys	Arg	Thr	Asp 270	Xaa	Leu
Сув	Arg	Ser 275	Arg	Leu	Ala	Asp	Phe 280	Xaa	Thr	Asn	Cys	Xaa 285	Pro	Xaa	Xaa
Arg	Xaa 290	Xaa	Thr	Xaa	Cys	Xaa 295	Ala	Xaa	Asn	Tyr	Xaa 300	Xaa	Cys	Leu	Xaa
Ala 305	Tyr	Xaa	Gly	Leu	Ile 310	Gly	Thr	Xaa	Met	Thr 315	Pro	Asn	Tyr	Val	Asp 320

Ser	Xaa	Xaa	Thr	Xaa 325	Xaa	Xaa	Val	Ala	Pro 330	Trp	Cys	Xaa	Cys	Arg 335	Gly
Ser	Gly	Asn	Xaa 340	Xaa	Glu	Glu	Cys	Glu 345	Lys	Phe	Leu	Xaa	Xaa 350	Phe	Xaa
Xaa	Asn	Pro 355	Суѕ	Leu	Xaa	Asn	Ala 360	Ile	Gln	Ala	Phe	Gly 365	Asn	Gly	Xaa
Asp	Val 370	Xaa	Met	Ser	Gln	Xaa 375	Xaa	Pro	Xaa	Xaa	Xaa 380	Xaa	Thr	Xaa	Ala
Xaa 385	Xaa	Xaa	Xaa	Xaa	Xaa 390	Arg	Val	Xaa	Xaa	Xaa 395	Pro	Xaa	Leu	Xaa	Xaa 400
Xaa	Xaa	Ser	Xaa	Xaa 405	Xaa	Xaa	Xaa	Xaa	Thr 410	Xaa	Val	Xaa	Xaa	Xaa 415	Cys
Xaa	Xaa	Xaa	Gln 420	Xaa	Gln	Xaa	Leu	Lys 425	Xaa	Asn	Xaa	Ser	Xaa 430	Xaa	Xaa
Xaa	Xaa	Cys 435	Xaa	Xaa	Xaa	Xaa	Xaa 440	Xaa	Xaa	Xaa	Xaa	Xaa 445	Xaa	Xaa	Xaa
Xaa	Xaa 450	Xaa	Xaa	Xaa	Xaa	Xaa 455	Xaa	Ser	Xaa	Xaa	Ala 460	Xaa	Xaa	Ser	Xaa
Xaa 465	Leu	Xaa	Xaa	Leu	Pro 470	Val	Leu	Met	Leu	Thr 475	Xaa	Leu	Xaa	Xaa	Xaa 480
Leu	Xaa	Xaa	Xaa	Leu 485	Xaa	Glu	Thr	Ser							

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